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REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 1 BG819678 LOCUS DEFINITION KEYWORDS SOURCE VERSION ACCESSION FEATURES ORGANISM source BG819678 653 bp mRN 602783172F1 NCI_CGAP_Brn67 5', mRNA sequence. BG819678 Email: cqapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10862 row: o column: 17 High quality sequence stop: 648. Enkaryota; Metazaa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Putheria; Primates; Catarrhini; Hominidae; Homo. 1 (hases 1 to 65%) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Homo sapiens ES. Unpublished (1999) Contact: Robert Strausberg, Ph.D. human. BC819678.1 G1:J4167265 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4934248" /clone_lib="NCI_CGAP_Brn67" /tissue_type="anaplastic oligodendroglioma with lp/19q Location/Qualifiers . 653 NA EST 22-MAY-2001 Homo sapiens cDNA clone IMAGE:4934248

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/note-"Organ: brain; Vector: pCMV-SPORT6; Site_1:
/ste_2: SalT; Cloned unidirectionally. Primer: Oli
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not
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Contact: Pomp, D
Department of Animal Science
University of Nebraska, Linco
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/lab_hos1-"DH10H (Life Technologies)"
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Norway rat.
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cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1788947
Seq primer: M13 Forward.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 8255
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                           thalamus, mid-brain, medulla, corpus Striatum, cerebral cortex and testis. The tag used to identify the source tissue is a string of 3-6 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. This library was then subtracted using a driver consisting of a mixture of all clones from UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, UI-R-C1, UI-R-C2 and UI-R-C2p."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="Laxon:10116"
/clone="U1-R-BT0"qk-h-03-0-U1"
/clone=lib="U1-K-BT0"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pTTT3D-Pac (Pharmacia) with a modified /note-"Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; This library (UI-R-BT0) consists of a mixture of individually tagged normalized libraries constructed from rat hippocampus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host-"DH108 (Lite Technologies)"
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                                                                                                                  Score 348.8; DB 11; Length 455; pred. No. 2.6e-87; 0; Mismatches 62; Indels 0;
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AJ003472
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Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Homo.
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/clone_lib-"Selected chromosome 21 cDNA library"
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoareséblue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is ikely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics (www.resgen.com) This clone is also
available through the I.M.A.G.E. Consortium at LLNL.
(info@inage.lln1.gov). IMAGE ID-1788947
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KST68B3 Athersys RAGE Library Homo sapiens
HG187HB0
                                                                                                                                                                                 Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
                                                                                                                                                                                                                                                          Harrington, J.J., Shert, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., bahl, T., Thornton, M., Kamachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElliqott, K., Clark, S., Mays, R., Smith, E. Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
                                                                                                                                                                                                                                                                                                                    Eukaryola: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.

1 (bases 1 to 487)
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                                                                                                                                                                                                                             Creation of Genome wide Protein Expression Libraries
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                HG187880.1
                                                                                                                       Athersys, Inc.
3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                               and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                                                     Duman
                                                                                          High quality sequence
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                                                                          scain@athersys.com
uality sequence stop: 487
[ocation/Qualifiers
/organism-"Homo sapiens"
/db_xrel-"taxon:9606"
/clome_lib-"Athersys RAGE Library"
/cell_line-"HT1080"
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pred. No. 3.6e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW529324 410 bp mRNA EST UT-R-BT1-akm-f-08-0-UI.S1 UT-R-BT1 Rattus norvegicus UI-R-BT1-akm-f-08-0-UI 3', mkNA sequence.
                                                                                                                                                                                                                 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
Rattus norvegicus
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AW529324.1 GI:7171738
EST.
                                                                                                                                               Fax: 319 335 9565
Email: msoareseblue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurogn. i; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                      discovery
                                                                                                                                                                                                                                                                                                                                                                      Normalization and subtraction: two
                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
                                                                                                               Research Genetics (www.resgen.com)
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
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            /strain="Sprague-Dawle
/db_xref="taxon:10116"
/clone-"UI-R-BT1-akm-f-08-0-U1"
                                                                              Location/Qualifiers
                                              /organism="Rattus norvegicus
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Pred. No. 2.1e-68;
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Expressed sequence tags from Xenopus unpublished (1999)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884
                                                                                                                                                                                                                     Amphibia, ... Xenopus. Xenopodinae; Xenopus. 1 (bases 1 to 427) 1 (bases 1 to 427) Schutz,K., de la Bastide,M., Huang,E.N., Na Schutz,K., spiegel,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW159035 427 bp mRNA
Za50e05 x1 Xenopus EST library
5', mRNA sequence.
AW159045 GI:6271064
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/lab_host="DHIOB" (Life Technologies)"
/loce="Vector: p773D-Pac (pharmacia) with a modified / note="Vector: p773D-Pac (pharmacia) with a modified / note="Vector: property of the library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, meanula, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest, eng. down. The subtraction has been previously in the property of the library from which this country is the property of the library from which this country is the property of the library from which this country is the property of the library from which this country is the property of the library from which this country is the property of the property of the library from which the previously the property of the library from which the previously the property of the library from which the property of the library o
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TAG_LI: UI-R-BT1
TAG_TI::UE-corpus-striatum
TAG_SEQ+CTAGG"
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/dev_stage="adult"
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No. 3.2
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plate: za50 row: e column: 05
seq primer: M13 universal forward primer
seq quality sequence stop: 427.
High quality sequence stop: 427.
                                     Danio rerio
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Rasborinae; C
                                                                                                                                                  MOLECULE. ;, mRNA sequence BG307959
                                                                                                                                                                              BG307959 483 bp mRNA EST 22-FEB-7001 fm55b04.y1 Zebrafish adult retina cDN\ Danio rerio cDNA cone 4199358 5' similar to TR:060469 06046') DOWN SYNDROME CELL ADHESION
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        Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
                                                                                                                     EST
                                                                                                                                       BG307959.1
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Hillier, L., Kucaba, T., Martin, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: Lambda Zap I: Site_1: XbaI: This library was supplied by Holly Cline (Cold Spring Harbor Labs). cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
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79.8%;
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Pred. No. 2.3e-65;
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 Beck, C.,
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Enteleostei;
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                                                               AGTACCACCGGACCAACCGTCTCACCGTGACCAAAAACCAACGACCACCTCCATCACGG
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Contact: Stephen L. Johnson
Contact Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
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WashU Zebrafish EST Project 1998
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Library constructed by: Susan E.
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/dev_stage-"1-2 years"
/lab_host*"E.Coli XL1-Blue MRF')"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_
ECORI; Site_2: Sall; This Zebrafish library was
constructed by Dr. Susan E. Brockerhoff (email:
sbrocker@u.washington.edu) RZPD library number: 760"
a 130 c 114 g 107 t
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/clone="4199358"
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/strain-"wild-type"
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Pred. No. 1.1e-60;
0; Mismatches 127;
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                                                          TCACACTAGAGTACAGGCCC-TTGGGACCACAG-TTGGACCACAGCTCAGAGGACCTCTC
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602019924F1 NCI_CGAP_Brn67 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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High quality sequence stop: 697.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 744)
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Ö.
                                                                                                                                                                                                                                                                                                                                                                                                /lab host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NC1_CGAP Library."
196 c 210 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="anaplastic oligodendroglioma with 1p/19q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4155508"
/clone_lib="NCI_CGAP_Brn67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.3%;
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Pred. No. 2.2e-60;
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RESULT 1
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CCGCCGCTGTGGAGCACCAAAGCCAGTTGATTGTCAGAGT
                                                                                                                                                                                                                                                                                                                                                                        al Similarity
277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: henkelg@aurorabio.com

pools of cells were isolated from a GenomeScreen(TM) library. The

pools of cells were isolated by retroviral integration of a gene

library of cells was generated by retroviral integration of a gene

togging element consisting of: 1) A promoterless beta-lactamase

proceeded by a splice acceptor as a reporter for gene expression;

2) A promoter driving neomycin resistance followed by a splice

denor to trap downstream exons. 3' RACE from neomycin gene was

denor to trap downstream exons. 3' RACE from neomycin gene was

portformed using total RNA from isolated pools. Output was shotgun

clared in pamp-1 and used to transform DH5-alpha competent

clared in pamp-1 and used to transform DH5-alpha competent

basteria. 5' ends of reported sequences were immediately preceded
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, Durick,K. and Pollok,B.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/cell_type-"Epithelial"
/cell_time "T47D"
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/db_xref-"taxon:9606"
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Methods in enzymology. 303, 19-44 (1999)
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1 (bases 1 to 1232)
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Ardi, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Hiraoka, T., Hori, F., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Immotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Immotani, K., Nonno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Sakai, K., Saho, H., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shibagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tayami, M., Tagawa, A., Shiraki, T., Sakai, K., Suzuki, H., Tayami, M., Tagawa, A., Shiraki, T., Sakai, K., Shibata, Y., Tayami, M., Tagawa, A., Shiraki, T., Sakai, K., Shibata, Y., Shibata, 
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                                                                                                                                                                                                         Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (USC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanayawa 230-0045, Japan (E-mail: yenome-rcs@qsc.riken.go.jp, URI:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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    cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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Genomic Sciences Center and Genome
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/protein_id="BAB29795.1"
/db_xre1="G1:12873613"
/translation="MCHTSGTCMPTGLCSSSLSPPPPSIALSTTMTISALQRTQPARS
GALTFASKQESGNPTESGMRIKGQCVATMLSLSASSPLQCRNTLASCLGRKTRSPSLQ
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/clone_lib-"kiKEN full-length enriched mouse cDNA library"
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/sex="male"
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/strain-"C57HL/6J"
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                                                                                                                                                                                                                                                                         Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
Hanagaki, T., Hara, A., Hayatsu, N., Hi amoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Izaw, M., Kato, H., Kazai, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Mammalia; Eutheria;
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Shehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseasc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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                                                                                                                                                                                                                  Direct Submission
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                                   gtgcattatcccctcctcggtggaggcgtacatcactgtcgtctcatgggagaaagacac
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GTGCCTCATCCCCTCTTCAGTGCAGGAATACGTTAGCGTCGTGTCTTGGGAGAAAGACAC
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CDNA library was prepared and sequenced in Mouse Genome EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer [5] GACAGAGAGGAGAGAGGACTCTTTTTTTTTTTTTTTVN 3/], cDNA was [6] GACAGAGAGGAGAGAGGACTCTTTTTTTTTTTTTTTVN 3/].
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1 366 c 349 g 297 t
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/db_xref-"taxon:10090"
/db_xref-"MGD:MGI:1903273"
/db_xref-"MGD:MGI:1918065"
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/sex="male"
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                 attgecetaaalggeegaateegaqtteteageaatgggtegttgetgateaaqeatqte 2268
                                                                                CGGGACCAGGATGGGATTTATGGCAAAGCAGTGATTCTCAATTGCTCTGCAGAGGGTTAT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (intoglimage.llnl.goy). IMAGE ID- 1799773 The following
repetitive elements were found in this cDNA sequence: 68-149,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
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University of Iowa
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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Norway rat.
Rattus norvegicus
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Seq primer: M13 Forward
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/lab_bost="bdf08" (Life Technologies)" with a modified /note="vector: pf7T3D-Pac (Pharmacia) with a modified /note="vector: pf7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Evo RI; The library polylinker; Site_1: Not 1; Site_2: Evo RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, (Idalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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/clone_lib="UI-R-BT1"
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/db_xref="taxon:10116"
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Pred. No. 3.1e-53;
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Contact: Yoshi. de Hayashizaki
Lahoratory for Genome Exploration Research Group. RIKEN Genomic
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BB336040 RIKEN full-length enriched, 10 days neonate medulla
oblongata Mus musculus cDNA clone B830046F24 3′ similar to AF217525
Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trehalose and its application for the synthesis of full length cDNA. Proc. Natl Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Carninct.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermosctivation of thermolabile enzymes by
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High-efficiency tull-length cDNA
19-44 (1999)
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/lab_host-"DH10B"
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                                                       /tissue_type="medulla oblongata"
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Sall; Site_2: BamHI; cDNA library was
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

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AAV31981 standard; cDNA; 6604 signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus cullosum agenesis; schizencephaly; diagnosis; assay; human; ds; ss. Human Down syndrome-ceil adhesion molecule DS-CAM1 cDNA ps-camt; bown syndrome-cell adhesion molecule; neural cell; (tirst entry) Location/Oualifiers 453..6185

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1320 1772	tgcccacgatcacgt	26 71	DЬ
1260 1712	aaaaggtggtgagtcc aaaaggtggtgagtcc	20 65	Qу
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1140 1592	tqqtraaaagtgacgg 	08 53	dd dy
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1020 1472	gcagcgtgacaggaact gcagcgtgacaggaact	96	Qy Db
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AAV31988

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atglugalantggctctctccttgltccagagcttcgcgaatgttttcagtgaagaccta

Matches

Similarity

100.0%;

Score 4678 Pred. No.

DB 2 19;

Length

6413; 0;

Gaps 60

0;

0;

Mismatches . 0 %

Conservative

Sequence

6413

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1633 A;

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C; 1707 G; 1292 T;

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other;

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cy question) clink library. Farther, cames were obtained by exon CC (respaint, and the complete PS CAM2 clink sequence was identified. CC DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) CC and is deleted for the entire transmembrane domain. The DS-CAM CS espans volo-1200 kb of genomic DNA and maps at chromosome CC 21q22.2-22.3. The invention also provides murian DS-CAM partial CC 21q22.2-22.3. The invention also provides murian DS-CAM partial CC companies (see AAV41985-87), expression vectors and host cells, and grangenic animals, antisense oligonucleotides, and primers useful CC ransgenic animals, antisense oligonucleotides, and primers useful CC associated with developmental and neurological DS-CAM polypeptides are CC associated with developmental and neurological processes. They can CC methods of repairing (regenerating) damaged or severed peripheral CC merves. The products can also be used in detection, diagnosis and CC therapy of developmental and neurological abnormalities such as CC compus callosum, or schizencephaly. Antisense oligonucleotides CC are used for inhibiting translation of mRNA.
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis;
                                                                                                                                                                                                                                                                                                                                                    DS-CAM2 (see AAM42087), an extracellular, soluble protein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and Plartificial chromosomes between ETS2 and MXI by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental and neurological abnormalities
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DS-CAM2 (see AAW42087),
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful ingene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic activity, activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constraints.
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Best Query Match

38.68;

Score 1806.8; Pred. No. 0;

DB 22;

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                                                                                                                                                                                                                            This cDNA sequence comprises the 5' region of a cDNA clone for murine Down syndrome cell adhesion molecule (DS-CAM), a member of a novel subclass of the 1g superfamily with homology to neural cell adhesion molecules. The middle region (see AAV31986) and 3' region (see AAV31987) of the clone are also provided. The murine DS-CAM clone was isolated from a C57 Black/6 mouse brain cDNA library using human DS-CAM cDNA (see AAV31981 and AAV31988) as
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                                                 cDNA library using numen by con con con concepts the invention also provides human DS-CAM proteins (see probe. The invention also provides human DS-CAM proteins (see ARW42086-87), as well as expression vectors and host cells. ARW42086-87), as well as expression vectors and host cells transgenic animals, antisense oligonucleotides, and primers useful consisted with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agencesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
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ethb0018f2; ss.
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by cloning in reporter gene vector without signal sequence,
transforming bacteria and mammalian cells, and identifying cells
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                                                                                                                                                                                                                                                                                                                                                                                                  This cDNA sequence comprises the middle region of a cDNA clone for murine Down syndrome-cell adhesion molecule (DS-CAM), a member of a novel subclass of the Ig superfamily with homology to neural cell adhesion molecules. The 5' region (see AAV31985) and 3' region (see AAV31987) of the clone are also provided. The murine DS-CAM clone was isolated from a C57 Black/6 mouse brain cDNA library using human DS-CAM cDNA (see AAV31981) and AAV31988) probe. The invention also provides human DS-CAM proteins (see AAV31986), as well as expression vectors and host cells, transgenic animals, antisense oligonucleotides, and primers usefu for amplification of DS-CAM nucleic acids. DS-CAM polypeptides a associated with developmental and neurological processes. They cassociated with developmental and neurological processes.
                                                                                                                                                                                                                                                                                                           associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (representating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as Down Syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
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CC for murine Down syndrome-cell adhesion molecule (DS-CAM), a member of a novel subclass of the 19 superfamily with homology to CC meural cell adhesion molecules. The middle region (see AAV31986) CC and 5' region (see AAV31985) of the clone are also provided. The CC murine DS-CAM clone was isolated from a C57 Black/6 mouse brain CC cDNA library using human DS-CAM come (see AAV31988) as CC probe. The invention also provides human DS-CAM proteins (see CAM42086-87), as well as expression vectors and host cells, CC transgenic animals, antisense oligonucleotides, and primers useful CC transgenic animals, antisense oligonucleotides, and primers useful CC associated with developmental and neurological processes. They can CC methods of repairing (regenerating) damaged or severed peripheral CC therapy of developmental and neurological abnormalities such as CC Down syndrome, mental retardation, holoprosencephaly, agenesis of CC the corpus callosum, or schizencephaly. Antisense oligonucleotides
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RESULT
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09-JUL-2000;
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                                                                                                                        The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nooLropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Inmune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                         Human Down syndrome-cell adhesion molecule DS-CAM probe E51.
                                                                                                                                                                                                                                                                                                            signal transduction; trisomy 21; mental reta
holoprosem ephaly; corpus callosum agenesis;
                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                        AAV31982;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAV31982 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178
                                                                                                                                                                                                                                                        W09817795-A1.
                                                                                                                                                                                                                                                                                                  schizencephaly; diagnosis; assay; human; ds;
                                                                                                                                                                                                                                                                                                                                       DS-CAM1; Down syndrome-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238
This polynucleotide comprises cDNA fragment E51 that was isolated from a human trisomy 21 toetal brain (14-wk gestation) cDNA library following a modified direct cDNA selection technique
                                                                 New isolated Down's Syndrome-cell adhesion molecule -develop products for detection, diagnosis and therapy developmental and neurological abnormalities
                                                                                                                                                                                                                                  30-APR-1998
                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                WPI; 1998-271791/24.
                                                                                                                                                                                    25-OCT-1996;
                                                                                                                                                                                                            23-OCT-1997;
                                             Example 2;
                                                                                                                                      Korenberg
                                                                                                                                                             (CEDA-) CEDAKS
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                                             79; 109pp; English
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                                                                                                                                                                                                                                                                                                                             mental retardation;
                                                                                                                                                                                                                                                                                                                                       molecule; neural cell;
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RESULT 10
AAH24799
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            applied to bacterial and P1 artificial chromosomes between ETS2 and MX1. E51 was used as a probe to screen the trisomy 21 foetal brain library. 62 Clones were isolated from the 2 million clones of the original library. Overlapping clones were obtained that were used to deduce a full-length sequence (see AAV31981) coding for novel Down syndrome-cell adhesion molecule DS-CAM1 (see AAW42086). A splice variant, DS-CAM2 (see AAV31988), was also identified. DS-CAM polypeptides are associated with developmental interface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and neurological processes.
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                                                                                                                                                                                                                                                                                                                                                  allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH24799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH24799 standard; DNA;
       Nucleic acids encoding 2 human cytokine receptor-like polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, cardiovascular and immune disorders -
                                                                                                                                                 03-DEC-1999;
                                                                                                                                                                                                07-JUN-2001
                                                                                                                                                                                                                         WO200140456-A1
                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                Ruben
                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                               .nflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                          igG Fc region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological processes. The polypeptides and nucleic acids used to develop products for the detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139;
                                                                         2001-367808/38
                                                                                                                                                                                                                                                                                                                                 c region; cytokine receptor-like protein; immune system disorder; mmatory disorder; immuno modulation; immune cell stimulation; gy; cancer; cardiovascular disorder; angiogenic disorder; healing; infectious disease; neural disorder; ss.
                                                            AAB84252
                                                                                                                                                                                                                                                                                                                                                                                                  sequence of a human cytokine receptor-like protein.
                                                                                               Ni J, Young
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inappropriate cytokine receptor protein expression. The polypeptides may also be used as antiquens in the production of antibodies, and in mayseys to identify modulators and inhibitors. Disorders that may be prevented, diagnosed and/or treated by the above methods include, for example immune system disorders, inflammatory disorders, immuno modulation, immune cell stimulation and proliferation, allergic reactions, aberrant cytokine receptor signalling and/or over expression of cytokine responses, cancers, cardiovascular disorders, angiogenic disorders, would healing and requireration, infectious diseases and
                                                                                                                                                                                                                                                                                                                 The present sequence encodes a human cytokine receptor-like protein. The cytokine receptor-like polypeptides and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                     neural disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                 237-238; 247pp; English.
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Sequence 3617 BP; 815 2.0%; A; 1182 C; Score 91.4; DB 22; Pred. No. 1.1e-15; 1016 <u>ი</u> 604 T; 0 Length other; 3617;

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qcgcaqqagacggggtcaggattgagcagatcttcacccggaccaaagaggatgttccag
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CCCCXXX
                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation; allergy; neurological disorder; Alzhelmer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma: skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angioqenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gastrointestinal disorder; pregnancy-related disorder.
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           AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode AAE01631-AAE01660 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                  WO200134623-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding partner identification; ss
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system disorder; AIDS; autoimmune disease; rheumatoid
                                                               Claim
                                                                                                                                                                                     Ruben
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                                                                                                                                                           2001-316490/33.
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2000US-0215137
proteins
                                                               457-459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; proliferative diso der;
                                                                                                                                                                                                                                                                                                                                                                       /partial
1297..1387
/*tag= b
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/note= "CDS does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental abnormality; haematopoietic disorder;
                                                                                           retinopathy
 and
                                                                                                                                                                                     GA,
                                                                                                      29 human secreted polypeptides, useful for and/or treating e.g. cancers, Parkinson's
                                                               535pp; English.
                                                                                                                                                                                                                                                                                                                                                              "Mature human secreted protein"
their genes
                                                                                                                                                                                        Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                           not
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not include start
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  are useful
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cc treating or ameliorating medical conditions, e.g., by protein or gene cc therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the presence of cc mutations in the new genes. Specific uses are described for each of the cc 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of cc annormalities, haematopoietic discours, foetal and developmental cc allergies, neurological disorders (e.g., rhematoid arthritis), inflammation, cc allergies, neurological disorders (e.g., Alzheimer's disease, cardiovascular disorders, sepsis, diseases of the immune system, cc ardiovascular disorders, appropriately, sepsis, disease, atherosclerosis, cc ardiovascular disorders, pregnancy-related disorders, anthona, asthma, cc kin disorders, and infections. The proteins can also be used to aid wound comburn, to maintain organs before transplantation, for supporting cell counture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used a aleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., ratioimmunoassay or enzyme linked communosorbent assay (ELISA). The present sequence represents a human secured protein-encoding CDNA of the invention.
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Matches Query Match Best Local Similarity 3152 3032 3209 qqqqlaaciiccaaliccaacalialcaaqigtcqacaqcaqcggggacagtgaggtttaca 3148 ccaycuur la---getcaccatcacygeggacggaggtcctgattggtccacctcagg 2968 AGCCCTTCACGTCCTACAAGTTCCCAAGTGAAGGCGACCAATGACATTGGCGACAGCGAGT 3093 accettectecacetaraycalceqealgtacyceaagaaceggattggcaagagegage 2911 daCalliqeaaaaiqqaattaleeqtqqetaeeaaafaqgttaeegagagtaeageaetg 3088 TCCTCTCCCTGACGCCCACACCACCACCTCCGTGCTAATCCGATGGCAGCCGCCAGCAG 2973 aagttcacctggagcctatalcatcacagagcatcagggtcacatggaaggctcccaaga 3028 ccqqcacqqqqccttcttctcaggaaatcatcaccaccactctcgaggatgtgcccagtt 3268 --CTTACCTACCTGAACAAGCACGCCGGTACCAGATACGGATGAGCGTGTACAACGCTG coctqqacaacctgaataaqttcactcaqtacqgcctggtggtggcaggcctgtaaccggg 3208 AAGGACT GAGGGGCTTTCACGCTTTCGAGGCATCAACAACCCAGGGGCCACATGGGCTGAG ACCIONALA LONALCIDO A LO CHECOTO CONTROCCIGATO COGATA COGGGAGO TIGOTATO TCAGCGAGGAGTCGGAG ccacactttccaaggaagccttgaatggaattctccaaggggttcagagtcatttactggg CAGCACCTCGTAACGTGGTCGTCCACGGCGCCACGGCCACACAGCTGGACGTGACTTGGG accccccgaaaatglccaagccatagcaacatcaccagaaagcatatcaatatcctggt 3328 AAGCCCAGCGGGGGAACCTCACAGAGCGAGTGAAGACGCTTTTCCTGGCTGAGAACAGCG TGGGTGAGGGGCCCTCCAGCCCCCCCGCAGGAGGTCTTTGTTGGGGGAGGCAGTGCCCACAG 388; Conservative 2.0%; 45.9%; INCTIGACCACCCTGCAGGCTGCCCCCGATGAAGCACCCACCA 3033 0; Score 91.4; Pred. No. 1 Mismatches 451; .3e-15 DВ 22; Indels Length 4336; 6; Gaps 2796 2852 2913 2616 3388 2676 2736

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27-AUG-1999;
11-JAN-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to the polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA1106899;
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                                                                                                                                                                                                                                               primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX KES
                                                                                                                                                                                                     Claim 1; SEQ
                                                                                                                                                                                                                                    and/or diagnosis of the full-length cDNAs -
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Best Local Similarity
Matches 313; Conserv
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                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs casally without any specialised methods. Anti31316 to AAH13628 and AAH13633 to AAH13642 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of the complementary to the compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 12218; 2537pp + CD ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95893 represent human amino acid sequences; and AAH13629 to represent oligonucleotides, all of which are used in the exemples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complementary strand of a polynucleotide which comprises a 5'-end
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Protein yrosine phosphate protein PTP-OB specifically expressed in bone cells - modulators of which are used to treat, e.g. osteoporosis, and prevent and treat bone loss and cancer.
                                                                                                                                                                                                                                                                                       PTP-OB; protein tyrosine phosphatase; osteoblast; differentiation; osteoclast; osteoporosis; bone; cancer; osteosarcoma; ss.
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                                                                                                                                                                                                                                                                                                            Protein tyrosine phosphatase' PTP-OB; PTP.psilon; osteoblast: recombinant protein; growth; differentiation; brain; human; s
                                                                                                                                                                                                                                                                                                                                                                                          Human protein Lyrosine phosphatase PTP-OB encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT85389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT85389 standard; cDNA;
                              19-AUG-1997
                                                                             US5658756-A
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es 227; Conserv
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nilarity 47.78;
Conservative
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                                                                                                                                                           Location/Qualifiers
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/*tag= a
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Pred. No. 3.1e:
0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an isolated and purified DNA molecule encoding human protein tyrosine phosphatase (PTP-OB) protein. The DNA is useful for production of the recombinant protein, which is a protein tyrosine phosphatase which may be involved in the growth and differentiation of osteoblasts and brain cells and is useful for identifying compounds that modulate PTP-OB activity and as a therapeutic agent for treating PTP-OH-related diseases.
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14-SEP-1993;
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P-PSDB; AAW27225.
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Maximum DB seq length: 200000000
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     Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-348-0068-6
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GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
                                                                                        NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEPAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1472 GTACACCATGTCGGACGGCACC 1493
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006H
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 126
CITY: RAHWAY
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                                               STRANDEDNESS:
                                                                              LENGTH: 6000 base pairs
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                                                           nucleic acid
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126 E. LINCOLN /
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                                 linear
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                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. WARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 189;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
                           TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2141 GTGCCCAGCGCGCCGCCGGAAGGTGGAGGCGGAGGCGCTCAACGCCACGGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gttccaggtcctcccgcgggtgtgaaggcagcggcggcctcagcctccatggtctt 3617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agttaccccccgaaaatgtccaagccatagcaacatcacc. ¬aagcatatccaatatcc 3324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttcacccgcgcaggagacggggtcaggagtgagcagatcttcacccggaccaaagaggat 3561
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   6000 base
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Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09158657 Patent No. 6214564
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: REFILENCE, SU JANE
TITLE OF INVENTION: CUNA ENCODING A NOVEL HUMAN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2021
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                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                        SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROBAN, GIDEON A.
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                          STREET:
                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                        E: Floppy disk

[BM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                           Release #1.0,
 08/800,825
                                                                       US/09/158,657
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Pred. No. 2.6e-09;
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                                                                                                           Version
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FILING DATE: 14-FEB-1997 ATTORNEY/AGENT INFORMATION:

NAME:

HAND,

J. MARK 14-FEB-1997

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-158-657-6
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PCT-US94-10166-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
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REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
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                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E.
                                                                                                                                                                                   APPLICANT: RODAN, GIDEON A
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                               2141
                                   COUNTRY: U. ZIP: 07065
COMPUTER READABLE FORM:
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TYPE: nucleic acid
STRANDEDNESS: Single
                                                                       STATE:
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Pred. No. 2.6e-09;
0; Mismatches 246;
                                                                                                               E. LINCOLN AVE
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US-08-427-497E-4

Sequence 4, Application Patent No. 5969124 GENERAL INFORMATION:

US/08427497E

APPLICANT: Lemmon, TITLE OF INVENTION:

Vance

A Method for Characterizing the

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Best Local Similarity 47.7%;
Matches 227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
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LENGTH: 6000 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W J111
REGISTRATION NUMBER: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-SEPT CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1721 TACGTGGTGGAGGACCTGAAGCCCAACACGGAGTACGCCTTCCGCCTGGCGGCCCGCTCG 1780
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TELEFAX: 138825
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                         3562 gttccaggtcotcccgcgggtgtgaaggcagccgcggcctcagcctccatggtctt 3617
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                                                                            CACACAGAGGTGGGACCAGGGCCGGAGAGCTCGCCCGTGGTCGTCCGCACGACGAGGAT 2140
                                                                                                      ttcacccgcgcaggagacgggqtcaggagtgagcagatcttcacccggaccaaagaggat 3561
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GTGCCCAUCGCGCGCGCGCAAGGTGGAGGCGGAGGCGCTCAACGCCACGGCCAT 2196
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TITLE OF INVENTION:

Nucleotide Sequence of L1CAM

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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                Matches
                                                                                                               Best
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Compaq Prolinea 5100e
OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
MEDIUM TYPE: storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: June 26, 19 ATTORNEY/AGENT INFORMATION:
                               1555 TATAGCTCCTACCACCTGGAGGTGCAGGCCTTTAACGGGGGGAGGATCGGGGGCCCGCCAGC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGIE TYPE: nucress
MOLECULE TYPE: nucress
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                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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ANTI-SENSE:
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3532 gagcagatetteaceeggaceaaagaggatgtteeaggteeteeegegggtgtgaaggea 3591
                                                   3472 tacaccaactacagcatccaggtgctggccttcacccgcgcaggagacgggggtcaggagt 3531
                                                                                                                                                                                                                                                       JOURNAL:
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CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/427,497E FILING DATE: April 24, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 0 FILING DATE: June 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                             Local Similarity
                                                                                                                                                                                                                         PAGES:
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                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: 17-18 week fetus
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                                                                                                                                                                                                                                           ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRY: U.S.A.
44114-2518
                                                                                                                                                                                                          : 416-423
1991
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S: Lemmon, Vance
Molecular structure and functional testing of human LlCAM: an interspecies comparison.
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E: Minnich & McKee
1100 Superior Avenue
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Characterized Thereby
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                                                                                                               Score 47.8; DB 2; Pred. No. 0.00063;
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TITLE OF INVENTION:
TITLE OF INVENTION:
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ANTI-SENSE: no
ORIGINAL SOURCE:
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FILING DATE: April 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/904,
FILING DATE: Jine 26, 1992
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CURRENT APPLICATION DATA:
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                   PUBLICATION INFORMATION:
AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
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                                                                                                            IMMEDIATE SOURCE
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STREET: Suite 700
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                                                                                                                             ORGANISM: homo sapiens INDIVIDUAL ISOLATE: 17
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                                                                                        LIBRARY:
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Molecular structure and functional testing
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Nucleotide Sequence of LICAM
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Best Local Similarity
Matches 119; Conserv
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Patent No. 5872225
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APPLICANT: Lemmon.
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TITLE OF INVENTION: A Met
TITLE OF INVENTION: Nucle
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TITLE OF INVENTION: Ch
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/90
FILING DATE: June 26, 19;
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: storable
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                          NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: CWR 2 149-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
                                                                                                                                                                                                                                              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
               TELEPHONE:
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DATE: 1991
RELEVANT RESIDUES IN SEQ ID
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OPERATING SYSTEM: DOS 5.0
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ZIP: 44114-2518
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STATE: Ohio
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                                                                                                                                                                                                          APPLICATION NUMBER: US/08/341,843B FILING DATE: No. 5872225ember 18, 1994
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(216) 980162
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6, 1992
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Pred. No. 0.00073;
""smatches 97;
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US-08-427-497E-1
                                                                                                                                                                                  Patent No. 5969124
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICANT: Lemmon, V
TITLE OF INVENTION:
TITLE OF INVENTION:
THE OF THE NOTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: Stratagene cDNA Library 936206 CLONE: synthesis of 4 clones PUBLICATION INFORMATION:
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LIBRARY: Strat
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MOLECULE TYPE: COM.
MOLECULE TYPE: COM.
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COMPUTER READABLE FORM
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                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Hlavin, Mary Louise AUTHORS: Lemmon, Vance
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                                                              STREET: 1100 Superior Avenue
STREET: Suite 700
CITY: Cleveland
                COUNTRY: U.S.A. ZIP: 44114-2518
                                                                                                                 ADDRESSEE: Fay, Sharpe, Beall, Fagan
ADDRESSEE: Minnich & McKee
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Pred. No. 0.00082;
0; Mismatches 97;
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RESULT 10
US-08-427-497E-2
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INFORMATION FOR SEQ ID NO: 1:
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OPERATING SYSTEM: DOS 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: CWR 2 149-3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
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CLONE: synthesis of 4 clones
PUBLICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J
                                                                                                                                                                          3592 geggeggeeteageeteeatggtetttgtgteetqgetteeeceteteaagetgaaegge 3651
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MOLECULE TYPE: nuclear I
MOLECULE TYPE: nuclear I
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                                                                     2839 GTGCTCACCGGCTACGTGCTCCTACCACCCCCTGGAT 2877
                                                                                          3652 atcatccgaaagtacactgtattctgctcccacccctat 3690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: Molecular structure and functional TITLE: testing of human LICAM: an TITLE: interspecies comparison.
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STRANDEDNESS: singl
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MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
INDIVIDUAL ISOLATE: 17–18 week fetus
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linear
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June 26, 1992
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Query Match 1.0%; Best Local Similarity 54.3%; Matches 119; Conservative

Score 47.8; DB 2; Pred. No. 0.00082; 0; Mismatches 97;

Length 3774; Indels

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; RELEVANT RESIDUES IN SEQ ID US-08-427-497E-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
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FILING DATE: APTIL 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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NAME: Minnich, Richard
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                                                                                                                                                                                                                        LIBRARY: Strat
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STREET: Suite 700
CITY: Cleveland
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                                                                                                                AUTHORS: Lemmon, Vance
TITLE: Molecular structure and functional testing
TITLE: human LICAM: an interspecies comparison.
                                                                                                                                                   AUTHORS: Hlavin, Mary Louise
AUTHORS: Lemmon, Vance
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INDIVIDUAL ISOLATE: 17-18 week tetus
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TOPOLOGY: linear
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                                  DATE:
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(216) 980162
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Minnich & McKee
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Nucleotide Sequence of L1CAM
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US-08-447-464-2
                                             Best Local Similarity 51.7 Matches 104; Conservative
                                                             Query Match
Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5690 base pairs
`3455 tggacgggctygaaaaglacaccaactacagcatccayqtgctygccttcacccgcqcag 3514
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-790-9090
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                      MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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                                                                                                                                                                                                                                                                                                  TELEPHONE: 212-869-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/1
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                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                    TOPOLOGY:
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                                                Score 45.8; DB 2;
Pred. No. 0.0044;
0; Mismatches 97;
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US-08-716-679-2
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Patent No. 5846800
                                                               Query Match
Best Local Similarity
Matches 104; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-PUS/MS-DOS
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2436 CACGGCAGAGAGTGTCATTA 2456
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APPLICATION NUMBER: US/08/130,570
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                3455 tggacquqctggaaaagtacaccaactacagcatccaggtgctggccttcacccgcgcag 3514
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CLASSIFICATION: 435
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TELEFAX: 55141 PENNIE
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TGGGCAGCCTGCTAGAGGATGAGACCTACACTGTGAGAGTGCTCGCCTTCACATCGGTGG 2315
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10036-2711
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nilarity 51.7%;
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                                                                 Score 45.8; DB 2;
Pred. No. 0.0044;
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                                                                                                                                                                                            Query Match
Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION_DATA:
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APPLICANT: Rabizadeh,
TITLE OF INVENTION: PI
TITLE OF INVENTION: PO
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MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
3264 cagttacccccccccaaaatgtccaagccatagcaacatcaccagaaaagcatatcaatatc 3323
                                                                                 3204
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                                                                                                                                  3144 ttacacectygacáacetyaataagtteacteagtacggeetggtggtggaggeetgtaa 3203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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                                                                     cogggocoggocoggggocottottotcaggaaatcatcaccaccactotcgaggatgtgoc
                                                                                                                TTATAAACTGGAAGGCCTGAAAAAATTCACCGAATATAGTCTTCGATTCTTAGCTTATAA 1805
                                                   TCGCTATGGTCCGGGCGTCTCTACTGATGATATAACAGTGGTTACACTTTCTGACGTGCC
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                                                                                                                                                                               Score 45.2; DB 4;
pred. No. 0.0058;
0; Mismatches 118;
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PCT-US94-05277-1
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PCT-US94-05277-1
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GENERAL INFORMATION:
                                                                                                      Query Match
Best Local Similarity
Matches 116; Conserv
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NAME: Kayan, Sarah A.
REGISTRATION NUMBER: 32,141
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
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                                       1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                       3144 ttacaccctggacaacctggataagttcactcagtacggcctggtggtgcaggcctgtaa 3203
                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                              POSITION IN GENOME
                                                                                                                                                                                                                                                                                                                  ORIGINAL SCHROET
                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: No
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CONA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/05277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20001
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                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                               CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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congacouqueseggggcottottotoaggaaatcatcaccaccactotogaggatgtgcc 3263
                                     TTATAAACTGGAAGGCCTGAAAAAATTCACCGAATATAGTCTTCGATTCTTAGCTTATAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinzler, Kenneth W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruskin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson, Karen
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                                                                                                         Conservative
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                                                                                                       Score 45.2; DB 5;
Pred. No. 0.0058;
0; Mismatches 118;
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                                                                                                                                           Length 4608;
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1806 TCC: TATEGTCCGGGCGTCTCTACTGATGATATAACAGTGGTTACACTTTCTGACGTGCC 1865

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US-08-986-485-1
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 610-407-0700
TELECA: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08986485 Patent No. 6046030
                                                                                                                                                                                                                                               Ouery Match 1.0%;
Best Local Similarity 50.9%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: WU, SHUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUBEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN 1.1G-1 HOMOLOG (HLIG-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: LHM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3324 ctyytccacactttccaaggaagccttgaatygaattctccaggggttcagagt 3377
                                                                                   2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1926 CTGGCTGCCTCCTCCATCAGGAACACAAAATGGATTTATTACCGGCTATAAAAT 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1866 AAGTGCCCCCCCCCCCAGAACGTCTCCCCTGGAAGTGGTCAATTCAAGAAGTATCAAAGTTAG 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3264 cagitaccccccgaaaaiqiccaagccatagcaacaicaccagaaagcatatcaatatc 3323
                                                                                                                                                                    2123 CCCCATCCTTGGTGGTCCCCCTTGGAAGACCGTGTGGTATCTGTGGGAGAAACAGTGGCCC 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                        731 tgccttgcaaaqcgctcgggcaccctgaqccagattaccgctggctgaaqqacaacatqc 790
                                                                                                                                                                                            671 ccccatr atactggatggqtttgaccatcgcaaag catggctqggcagcgtgtggagc 730
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                                                                                     TCCAATGCAAAGCCACGGGGAACCCTCCGCCCCGCATCACCTGGTTCAAGGGGGACCGCC 2242
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linear
                                                                                                                                                                                                                                                   0;
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Search completed: March 4, 2002, 05:11:29 Job time: 16943 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

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ALIGNMENTS

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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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18.4
17.4
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seq length: 2000000000
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Match Length
 100.0
92.0
87.0
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87.0
84.0
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20
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Gapop 10.0 , Gapext 1.0
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BG383716
BG348199
BI102963
CNS025H0
AW176762
AV158019
AI422998
            AW780736
N24917
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 BF348620 602019924
BG383716 301966 MA
BG34-L199 dg39c10.y
BI102963 602888573
AL182061 Tetraodon
AW176762 RCO-CT009
AV158019 AV158019
AI422998 tf31b11.x
AI927023 wo87a06.x
AW780736 5184766.y
NZ4917 yy01h12.s1
AW015308 UI-H-BIO-
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AQ339036 HS_5021_A BF391154 UI-R-CA1-	AQ339036 BF391154	312 13 374 11	82.0 82.0	16.4	4 2
AA694519 ah35h05.s			2.0	თთ	40
AL410504 T3 e			4.0	0	39
BE253944 6011			4.0	6	38
Ō	BI4:		4.0	σ,	37
異性	A073		4.0	שפ	υ ω ω
3 0	BI14		4.0	5	34
g			4.0	6	3
7	AZ27226		4.0	9	32
g	BG48091		4.0	5	31
≥	AU00534		4.0	σ.	30
AZ717126 RPCI	AZ71712		4.0	σ.	29
BG751248 6027	BG75124		4.0	5	28
AW348296 GM21	AW34829		4.0	5	27
AQ307774 HS_2	AQ30777		4.0	σ.	26
AA160797 zo60	AA16079		4.0	σ.	25
B1426424 sag03a12.	BI42642		.0	ᡣ	24
AQ150756 HS_3	AQ15075		4.0	σ.	23
=	AZ36373		4.0	5	22
636091 tz	A163609		4.0	ŗ	21
229092 RP	AZ22909		4.0	ç۰,	20
188488	AA18848		4.0	.5	19
363648	AZ 3		4.0		18
89448	AQ89448		.0	.5	17
148002	AA20084		4.0	.5	16
AQ996872 RPCI	AQ99687		٠.٥	.5	15
347190	AI34719		4.0		14
4007 C840	C84007		4.0	٠,	13

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION RESULT BF348620 FEATURES COMMENT JOURNAL source BE348520 : 4 bp mRNA EST 22-NOV-2000 60201:924F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155508 5', mRNA sequence. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9426 row: p column: 05 High quality sequence stop: 697. Location/Qualifiers. Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL) Mammalia; Eutheria; Prin. + +--; Catarrhini; 1 (Lases 1 to 744) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Unpublished (1999) Contact: Robert Strausberg, Ph.D. Homo sapiens Eukaryota; M BF348620 BF348620.1 GI:11296215 human /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4155508" /clone_lib="NCI_CGAP_Brn67" tissue_type="anaplastic oligodendroglioma with lp/19q/ Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Prim. + --; Catarrhini; Hominidae; Homo. Gene Collection (MGC) þe

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BASE COUNT
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ORGANISM
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ORIGIN
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Вb
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Best Local S
Matches 20
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Best Local :
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                                                           Matches
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 178
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CCAGTTCTTAAAGGAGCAGG
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301966 MARC 1PIG Sus s
BG383716
BG383716.1 GI:1330818
                                                           l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                   Bmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called
v0.980904.e. Vector identified by cro
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO Box 166, Clay (Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 88 row: K column: 9
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                      PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ARS, US Meat Animal Research Center
ox 166, Clay Center, NE 68933-0166, U
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B (T1 phage-resistant)",
/note="Organ: brain; Vector: pCMV-SPORFS; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 196 c 210 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith TPL
                                                                                                                                                 /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
150 c 120 g 170 t
                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                            /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                            ∕organism≖"Sus scrofa"
                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No.
                                                                                         Score 18.4;
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cross_match with the -minscore 18
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KEYWORDS
SOURCE
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                                                                           Query Match
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Washu Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG348199 442 bp mRNA EST dg39c10.yl Xenopus laevis gastrula non normalized cDNA clone IMAGE:3751290 5', mRNA sequence.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xinngaOlie19
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Other_ESTs: dg39c10.x1
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       l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: -40RP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertobrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library constructed by Bruce Blumberg
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/clone_liba_sassisticle
/lissu_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host_"Top-10 F'"
/lab_host_"Top-10 F'
/lab_host_"Top
                                                                                                                                                                                                                               library."
a 105 c
                                                                                                                                                                                                                                                                                                           contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 1111-1120). Note: This is a Xenopus Gene Collection (XGC)
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                                       87.08;
94.78;
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   Score 17.4; DB 11;
Pred. No. 3.8e+02;
0; Mismatches 1;
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4; νω
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SOURCE
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                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                     Eukaryota; Metazoa; Chordata; Crania a; Vertebraia; Ente ostomi; Actinopterygii; Neopterygii; Teleostri; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                 Weissenbach, J.
                                                                           1 (bases 1 to 832)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
                                                                                                                                                                                                                             GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                       CNS025H0 832 bp DNA GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 236Jl6 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
18; Conser
                                                                                                                          Tetraodontidae; Tetraodon.
                                                                                                                                                                                                       Tetraodon nigroviridis
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Plate: LLAM11120 row: a column:
High quality sequence stop: 737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
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1 (bases 1 to 739)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BI102963.1 GI:14553856
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                                                            L., Billault, A., Quetier, F., Saurin, W.,
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/clone="IMACE:5043738"
/clone=!b="NGLCGAP_Kid14"
/clone=Lib="NGLCGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NGLCGAP Library. | "
a 201 c 168 g 170 t 1 others
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/strain="FVB/N"
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Pred. No. 3.9e+02;
Prematches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 739;
                                                              Bernot, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer: Oligo dT
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                                                                             Fisher, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ccagttctcaaaggagcag
                                                                                                                       This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.p1?t1-RC0&t2-RC0-CT0094-200899-002-B12&t3-1999-08-20&t4-1)
Seq primer: puc 18 forward High quality sequence stop: 177.
                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                  Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                        Brazi
                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                   Umpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                            The FAPESP/LICE Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                  HCGP http://www.ludwig.org.br/ORESTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW176762 177 bp mRNA EST 16-NOV-1999 RC0-CT0094-200899-002-B12 CT0094 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of
scale clone-end sequencing project of the Tetraddon nigroy
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracolon nigroviridis DNA sequence
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                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0094"
       /note="Organ:
                       /dev_stage="Adult"
                                                                                                                 Location/Qualifiers
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/clone_lib="G"
/note="Genoscope sequence ID : COAG236DE08SP1-end
PUC-Ori"
221 c 168 g 202 t 5 others
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/db_xref-"taxon:99883"
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Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara Akahira,S., Nojima,Y., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Nuramatsu,M., Okazaki,Y. and Hayash 'Aki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV158019 Mus musculus head C57BL/6J 12-day embryo Mus musculus cDNA
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           18;
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Contact: Chie Owa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Tharaki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@rtc.riken.go.jp
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                                                                                                                                                                                                                                                                                                                                  details
                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3010012H19"
                                                                                                                        /tissue_type="head"
/dev_stage="12-day embryo"
64 c 70 g 121 t
                                                                                                                                                                                               /clone_lib-"Mus musculus head C57BL/6J 12-day embryo"
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                              /sex="mixed"
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               Score 16.8; DB 10;
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les 18; Conservative
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1 (bases 1 to 334)

1 (NINDS-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1588 Std Error: 0.00
Seg primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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AT927023 343 bp mKNA WO87a06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
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78 c 95 g 76 t
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Pred. No. 7.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                         Length 334;
                                                                                                                                                                                                                    Indels
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                 IMAGE: 2462290
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                                  08-MAR-2000
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by Bento
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., I
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., I
                                                                                                                                                                                                                                                                                                                             AW780736 350 bp mrnn EST 112-MAY-2000 12-MAY-2000 EST 5184f06:y1 Gm-c1037 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1037-732 5', similar to TR:096305 Q96305 SIMILAR TO CLUTAREDUXIN ENCODED BY GENBANK ACCESSION NUMBER Z49699 ;, mrnn sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                        EST
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Insert Length: 444 Std Error: 0.00
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AW780736.1
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                               (bases 1 to 350)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: kidney; Vector: p7773D-Pac Pharmacia) with a modified polylinker; Site_1: Not I; Si _2: Eco RI; Plasmid DNA from the normalized library HCl_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Spares and M. Fatima Bonaldo. "B c 97 g 80 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Kid11"
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Pred. No. 7.1e+02;
0; Mismatches 2;
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Best Local Similarity
Matches 18; Conserv
                                                     AUTHORS
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
                                                                                                                                                                                                                                                                           N24917 356 bp mRNA EST 28-DEC-19901h12.S1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE: 270023 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0010 or (314) 427-3322 AX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
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Public Soybean EST Project
                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into eqenomesystems.com web site: www.genomesystems.com
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314 286 1810
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/clone_lib."Cm-c1037"
/tissue_type="fully expanded leaves of greenhouse grown plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells. This library was constructed in the laboratory of Dr. i.lla Vodkin by Anu Khanna at the University of Illinois at Urbana- Champaign. email: 1-vodkin@uiuc.edu" 46 c 65 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inkers adapters were ligated to the blunt ended cDNA fragments; followed by NotI digestion. The CDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli Electro- Max DH10B host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restrictions site. SalI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vertor: psport; Site_1: Not; Site_2: Sali; This cDNA library was constructed from mRNA isolated from fully expanded leaves of greenhouse grown plants that were 2 weeks old. The library was prepared using the Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage-"2 week old"
/lab_host-"DH10B"
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/db_xret-"taxon:3847"
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                                                                                                Chordata;
Primates;
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Pred. No. 7.1e+02;
                                                                                                     Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ccagttctcaaaggagcagg
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: MCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                  AW015308 358 bp mRNA EST UI-H-BIO-aap-e-04-0-UI.sl NCI_CGAP_Subl Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
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AW015308.1 GI:5864065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,R., Williamson,A., Wohldman The WashU-Merck EST Project
                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 358)
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h quality sequence stop: 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organisma"Homo sapiens"
/db_xref="CDB:3879665"
/db_xref="taxon:9606"
/clone="IMAGE:270023"
/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 7.1e+02;
0; Mismatches 2;
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                                                                                                                                                          ACCESSION
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                                                                                                                                                                                                                                              RESULT 13
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                                    AUTHORS
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Williams,J.,
                                                                                                                          EST
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156 CCAGTCCCCAAAGGAGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                               C84007 359 bp mkNA EST 28-APR-1999 C84007 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSC227, mRNA sequence.
                                                                                                                Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
1 (bases 1 to 359)
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Seq primer: M13 Forward
                                 Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
                                                                                                                                                                                                                                         Dictyostelium discoideum.
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NCI_CGAP_PC21. NCI_CGAP_LSB. NCI_CGAP_CO14. NCI_CGAP_CO15.

NCI_CGAP_Kid15. NCI_CGAP_Kid12. NCI_CGAP_CO15.

NCI_CGAP_CLL11. NCI_CGAP_LSB. NCI_CGAP_BC24. NCI_CGAP_CO3.

NCI_CGAP_CLL12. NCI_CGAP_LSB. NCI_CGAP_BC23. NCI_CGAP_CO3.

NCI_CGAP_CLL12. NCI_CGAP_LSB. NCI_CGAP_BC24. NCI_CGAP_GC6.

NCI_CGAP_CLL12. NCI_CGAP_LSB. NCI_CGAP_BC24. NCI_CGAP_GC6.

NCI_CGAP_CLL24. NCI_CGAP_LSB. NCI_CGAP_BC24. NCI_CGAP_GC6.

NCI_CGAP_CL125. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_GC6.

NCI_CGAP_CL12. NCI_CGAP_LSB. NCI_CGAP_CSB. NCI_CGAP_LSB. 
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19 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_LIB-NCI_CGAP_Pr22
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Pred. No. 7.1e+02;
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Takeuchi, I., Ochiai, H. and Tanaka, Y.
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University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage
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DNA Res. 5 (6), 335-340 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI347190 380 bp mRNA EST 08-APR-1999 tc04g04.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062902 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AI347190
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1 (bases 1 to 380)
                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 529 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 337.
                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan.
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/clone="SSC227"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
57 c 68 g 119 t 1 others
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                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2062902"
/clone_lib="NCI_CGAP_Co16"
/note="Organ: colon; Vector:
modified polylinker; Site_1:
                                                                                                                                                                          Location/Qualifiers
                                     /tissue_type="colon tumor, RER+"
/lab_host="DH108"
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Pred. No. 7.1e+02;
0; Mismatches 2;
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      pT7T3D-Pac (Pharmacia) with
Not I; Site_2: Eco RI;
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AQ996872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ996872 380
RPCI-23-383015.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sha, B., Levins, M., Mcyann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
1 (bases 1 to 380)
                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from kesea ch Genetics (info@resgen.com). BAC end page: http://www.liur.oru/ldb/hac_ends/mouse/bac_end_intro.html plate: 383 row: o column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                            Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid DNA from the normalized library NC1_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1143351). Subtraction by Bento Soares and M. Fatima Bonaldo. a 93 c 108 g 87 t
                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-383015"
/clone_lib="RPCI-23"
/note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or Brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                            1. .380
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                      /sex="Female"
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90.0%;
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RPCI-23 Mus musculus genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MD 20850, USA
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ORIGIN

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Run
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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1: /SIDS2/gcgdata
2: /SIDS2/gcgdata
3: /SIDS2/gcgdata
              ## SIDS2/gcgdata/geneseq/yeneseqn/NA198 JAT: *
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SIDS2/gcgdata/geneseq/geneseqn/NA199 JAT: *
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Gapop 10.0 , Gapext 1.0
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/SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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29.632 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

kesult No.	Score	Query Match	Query Match Length DB		JD	Description
_ ;	20	100.0	20	19	AAV31983	Human Down syndro
2	20	100.0	6413	19	AAV31988	Human Down syndron
اب	20	100.0	6604	19	AAV31981	Human Down syndrom
4	18.4	92.0	2173	19	AAV31987	Mouse Down sync
_U	18.4	92.0	54548	21	AAZ45596	DNA sequence of
c 6	17.4	87.0	2197	21	AAZ89617	A. sydowi atl-S
c 7	16.8	84.0	187	16	AAT22739	Human gene signatu
c 8	16.4	82.0	12923	10	AAN90338	Sequence of hun
ာ 9	15.8	79.0	209	22	AAI25968	Probe #15901 to
c 10	15.8	79.0	209	22	AAI53359	Probe #22045 us
ဂ 11	15.8	79.0	563	ر د	AAI16773	Probe #6/06 to:

New isolated hown's Syndrome-cell adhesion molecule develop products for detection, diagnosis and therapy

used ç WPI; 1998-271791/24. Korenberg JR

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AAH15260 AAF30955 AAH16558 AAA61272	AAH42469 AAH42469 AAC43700 AAS22645 AAF27735 AAF27735 AAF27881	AA157849 AA157849 AAA49173 AAX81466 AAX81465 AAX81465	AAH05981 AAH14284 AAX20577 AAC76989 AAC68502 AAH09066 AAH19066 AAH51608 AAH318475 AAH38475	AA140280 AA148672 AA108987 AAH00627 AA135523 AA1135523 AAA118697 AAV152299 AAH13400
immul	Nucleotide sequenc 2ea mays DNA fragm Human cDNA encodin Human transport pr Human cDNA sencodin	Human polynucleoti toDNA encoding huma Mosaic flaA gene c Mosaic flaA gene c Mosaic flaA gene c Mosaic flaA gene c	E	Probe #8966 used t Probe #17358 used t Probe #8978 used t Enterococcus avium Probe #4209 used t Probe #3980 used t Human cDNA sequenc Streptococcus pneu

ALIGNMENTS

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RESULT
AAV31983
DS-CAM1; hown syndrome cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; PCR; primer; SS.
                                                                                                                                                                                                                                            Human Down syndrome-cell adhesion molecule DS-CAM primer B9-131F
                                                                                                                                                                                                                                                                 28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                    AAV31983;
                                                                                                                                                                                                                                                                                                       AAV31983 standard; cDNA; 20 BP.
                                                                                                       23-OCT-1997;
                                                                                                                           30-APR-1998.
                                                                                                                                              W09817795-A1
                                                                                                                                                                            Synthetic.
                                                                                     25-OCT-1996;
                                                                                                                                                                Homo sapiens
                                                                 (CEDA-) CEDARS SINAI MEDICAL CENT
                                                                                     96US-0029322
                                                                                                        97WO-US19547
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RESULT
AAV31988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forward primer B9-131F and reverse primer B9-131R (see AAV31984) were used in RT-PCR assays of cDNA libraries of various human tissues to determine human Down syndrome-cell adhesion molecule DS-CAM (see AAV31981 and AAV31988) expression. The results demonstrated expression of human DS-CAM mRNA in foetal and adult brain, and foetal kidney. In addition, a breast carcinoma cell line showed expression of human DS-CAM mRNA. DS-CAM polypeptides (see AAW42086-87) are associated with developmental and neurological processes. The polypeptides and nucleic acids are used to developmental products for the detection, diagnosis and therapy of developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ches_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 79; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV31988 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and neurological abnormalities
Whis cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging to a novel subclass of the 1g superfamily with highest homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                 holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DS-CAM2; Down syndrome-cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV31988;
                                                                                                                                                                                                                                                                       23-OCT-1997;
                                                                                                                                                                                                                                                                                                 30-APR-1998
                                                                                                                                                                                                                                                                                                                           ₩09817795-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                              Claim
                                                                                      New isolated Down's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
                                                                                                                                             WPI; 1998-271791/24.
P-PSDB; AAW42087.
                                                                                                                                                                                      Korenberg
                                                                                                                                                                                                                (CEDA-) CEDARS SINAI MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 BP; 6 A; 5 C; 6 G; 3 T; 0 other;
                                                               83-90;
                                                                                                                                                                                                                                             9605-0029322
                                                                                                                                                                                                                                                                       97WO-US19547.
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 453..5168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA; 6413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                               109pp;
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                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DH pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DH 19; Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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trapping, and the complete DS-CAM2 cDNA sequence was identified. DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) DS-CAM2 is a splice variant of membrane-bound DS-CAM2 (see AAW42086) DS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and P1 artificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk
                                                                                                                                                   therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agenesis the corpus callosum, or schizencephaly. Antisense oligonucleoti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gestation) cDNA library.
Sequence 6414 BP; 1633 A; 1781 C; 1707 G; 1292 T; 0 other;
                                                                                                        used for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Further clones were obtained by exon
                                                                                                                                                                         Antisense oligonucleotides
                                                                                                                                                                                                                                           of
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Matches Query Match Best Local Local Similarity 20; Conservative 100.0%; 100.0%; 0; Score 20; Pred. No. Mismatches DB 19; 2.7; 0; Length 6413; Indels 0; Gaps

0

RESULT AAV31981 w

4877 ccayttctcaaaygagcagg

1 ccaqttctcaaaggagcagg

20 4896

δõ B

AAV31981 standard; CDN/ 6604 48

28-SEP-1998 (first entry)

Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.

DS-CAMI; Down syndrome-coll adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation; schizencephaly; diagnosis; assay; human; holoprosencephaly; corpus callesa. ...prinesis;

Homo sapiens

Key mat_peptide sig_peptide /*tag- 8 /*tag-522..61 /*tag-Location/Qualifiers 453..6185 ..6162

WO9817/95-A1

30-APR-1998

23-OCT-1997;

97WO-US19547

25-0CT-1996; 96US-0029322

(CEDA-) CEDARS SINAI MEDICAL CENT

Korenberg

WPI; 1998-271791/24

P-PSDB; AAW42086

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ALSULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc gestation) cDNA ilbrary. Further clones were obtained by exon cc trapping. The complete DS-CAM1 cDNA sequence was deduced from CC overlapping clones. A splice variant cDNA (see AAV31988), encoding commembrane bound DS-CAM2 (see AAW42087), was also identified. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome CC 21q22.2-22.3. The invention also provides murine DS-CAM partial CC sequences (see AAV31985-87), expression vectors and host cells, cc and separation of DS-CAM nucleic acid. D:-CAM polypeptides are CC associated with developmental and neurologic | processes. They can complete the set of the capy of developmental and neurologic | processes. They can complete the set of the corpus callosum, or schizencephaly. Antisense oligonucleotides are clown syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides are closed for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and Pl artificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAMI (see AAW42086), a cell surface glycoprotein belonging to novel subclass of the Ig superfamily with highest homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 65-72; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4877 ccagiteteadaggageagg 4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Down's Syndrome-cell adhesion molecule - us develop products for detection, diagnosis and therapy of
                                                                                                                                                                                                                                signal transduction; trisomy 21; mental reta
holoprosencephal; corpus callosum agenesis;
schizencephaly; diagnosis; assay; mouse; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV31987 standard; cDNA; 2173 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6604 BP; 1673 A; 1827 C; 1768 G; 1336
                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                                                  DS-CAM; Down syndrome-cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation;
               (CEDA-) CEDARS STNAI MEDICAL CENT
                                                                                                                                                            W09817795-A1
                                                                                                                                                                                                                                                                                                                       Mouse Down syndrome-cell adhesion molecule DS-CAM 3' cDNA.
                                                                                                                                                                                                                                                                                                                                                               28-SEP-1998
                                                                                        23-OCT-1997;
                                                                                                                          30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ccagt Leteauaggageagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                    96US-0029322
                                                                                        97WO-US19547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (14-wk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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0;

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Q
                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                 transgenic animals, antisense oligonucleotides, and primers useful for amplification of INS-CAM nucleic acids. DS-CAM polypeptides are associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (requerrating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                  neural cell adhesion molecules. The middle region (see AAV31986) and 5 region see AAV31985) of the clone also provided. The murine DS-CAM clone was isolated from a C57 Black/6 mouse brain cDNA library using huma. DS-CAM cDNA (see AAV31981 and AAV31988) probe. The invention also provides human DS-CAM proteins (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
                                                                                                                                                                                                                          therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                             probe. The invention also provides numerican process.

AAW42086-87), as well as expression vectors and host cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             member of a novel subclass of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-271791/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Korenberg
                                                                                                                                                                          Sequence 217 + BP;
                                                                                                                                                                                                            are used for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for murine Down syndrome-cell adhesion molecule (DS-CAM), a
cDNA sequence comprises the 3' region of a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Page 81-83; 109pp; English
                                                                                Conservative
                                                                                                                                                                            585 A; 598 C;
                                                                                                92.0%;
95.0%;
                                           20
                                                                                0;
                                                                                                    Pred. No.
                                                                                                                   Score 18.4;
                                                                                Mismatches
                                                                                                                                                                            554 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The middle region (see AAV31986)
The middle region (see AAV31986)
The management of the middle region (see AAV31986)
                                                                                                                                                                            436 T;
                                                                                                      14;
                                                                                                                   DB 19;
                                                                                                                                                                            0 other;
                                                                                Ξ.
                                                                                                                     Length
                                                                                  Indels
                                                                                                                       2173;
                                                                                0;
                                                                                Gaps
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RESULT
AAZ45596
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 Human; PCNG4 region; X chromosome; q13 region; polymorphism; mental retardation; autism; depression; bipolar affective disorder; hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                               DNA sequence of the wild type human PCTG4 region of Xql5.
                                                                                                                                                                                                                                   06-APR-2000
                                                                                                                                                                                                                                                      AAZ45596;
                             exon
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                         AAZ45596 standard; DNA; 54548
                                                        promoter
                                                                                     promoter
                                                                                                                                                                                                                                                                                           ر
ح
                                                                                                                                                                                                                                  (titst entry)
                                                     complement (1565..1815)
                                                                                             /note= "human OPA exon"
                           2008..2112
                                                                  /*tag= b
/note= "human
                                                                                     1398..1648
                                                                                                                                   Location/Qualifiers
                                     /note- "unknown
                                                                                                                            1391..1490
/note= "human OPA promoter"
         /mamber-
                   /*tag=
                                              /*tag=
                                                a
                                                                 OPA promoter"
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7 7 7																
e von	exon	exon	exon	exon	exon	uoxe	exon	exon	exon	exon	exon	exon	exon	exon	exon	exon
	/"Lag- " /number= 19 /number= 19 /note= "human OPA promoter" 96069769 /*tag= v	91	/ Lag = 17 / number = 17 / note = "human OPA promoter" 8674.8792 /*tag = t	r=	8 . 7	77	7	<pre>/*tag= n /number= 12 /note= "human OPA promoter" 67987027 /*tag= 0</pre>	/*tag- m /*tag- m /note- "human OPA promoter" 62336359	/note- "human OPA promoter" 53775513 /*tag- 1 /number= 10 /note- "human OPA promoter" 6724 6666	OPA	J. 66 7 L	4 7	/*teg= 9 /number= 5 /note= "human OPA promoter" 39624072	/*tag- f /number- 4 /note- "human OPA promoter" 3608.3787	<pre>/*tag= e /number= 3 /note= "human OPA promoter" 26492805</pre>
												•				
				FT ex					PT ex							
FT exon	FT exon	FT exon	FT FT exon	FT exon	FT exon FT FT	FT exon FT FT	FT exon FT FT	FT FT exon FT		FT exon FT exon			E.I. exou	FT FT exon FT exon	FT FT exon	FT exon
exon 20207	exon	/note= /note= 19525. /*tag=	/number	exon	exon	/note- exon 16999. /*tay-	/note= exon 15765 /#tag=	exon	exon	exon 1	exon 12672 	exon 12317 /number/ /number/ /number/ /number/	/number /note= exon 11751 /*tag=	/number /note= exon 11235 /*tag-	/number /note= 'exon 10933 /*tag=	/number /note= exon 10530
exon (4.1.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	/note= "} exon 198320 /*tag= a	/note= "} /note= "} exon 195251s /#tag= /number=	exon	/note- "h 1773617 /*tag= a	exon	/note- exon 16999. /*tay-	/note= "r /note= "r 1576515 /*tag= a /number-	/number /note= exon 15487 /*tag= /number	exon 1	exon 14187 /*tag- /number /number /note- exon 14710	Proces	/number 23 /note	/number* /note= "h 1175112 /*tag= a	/number- /note- "I exon 1123511 /*tag- 2	/number= /note= " 'exon 10933' /*tag=	/number= /note= " 105301 /*tag=

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 RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                            promoter
Novel DNA encoding Aspergillus fructosyl transferase useful for production of polyfructose which is used to manufacture surfacts suspension agents .
                                                                                                                                                                                             Aspergillus sydowi.
                                                                                                                                                                                                              viscosity;
                                                                                                                                                                                                               Fructosyl transferase; af1-SST;
viscosity; sedimentation; food;
                                                                                                                                                                                                                                                                      AAZ89617;
                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                        09-MAR-2000.
                                                                                                                                       DE19840028-A1
                                                                                                                                                                                                                                                      23-JUN-2000
                                                                                                                                                                                                                                                                                      AAZ89617 standard;
                                 WP1; 2000-257741/23
P-PSDB; AAY51947.
                                                                                         02-SEP-1998;
                                                                                                         02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                      1 ccagttctcaaaggagcagg 20
                                                                                                                                                                                                                                      sydowi
                                                                                                                                                                                                                                                                                                                                                                             Match
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                                                                                                                                                                                                                                                                                                                                                              l Similarity
19; Conser
                                                                         MAX PLANCK GES FOERDERUNG
                                                                                                                                                                                                                                       afl-SST cDNA
                                                          Rehm J,
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                       (first entry)
                                                                                        98DE-1040028
                                                                                                         98DE-1040028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= aq
/number= 41
/note= "human
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "human OPA promoter"
26123..26275
/*tag= _au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23878..24018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "human
23283..23505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "human OPA promoter"
20372..20590
                                                                                                                                                      /*rag= a
/product= "afl-SST"
                                                                                                                                                                                                                                                                                                                                                                                                                                             24823..25096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24531..24612
                                                                                                                                                                        21..2069
                                                                                                                                                                                                                                                                                                                                                                                              /note= "probable NL-3 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number≖ 40
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             /number≖
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note≖ "human OPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                       cDNA; 2197
                                                         Wendenburg
                                                                                                                                                                                                                                                                                                                                                                     92.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aı
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                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                              Score 18.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPA
                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                polyfructose; surfactant manufacture; ss.
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter"
                                                                          WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                       No. 19;
          to manufacture surfactants
                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                               1:
                                                                                                                                                                                                                                                                                                                                                                              Length 54548;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                Gaps
           and
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RESULT 7
AAT22739/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel nucleic acid molecule (I) encoding a fructosyl transferase isolated from Aspergillus sydowi. The fructosyl transferase is useful for the production of polyfructose. Polyfructose can be used to manufacture surfactants, to increase the viscosity of an aqueous system, as a suspending agent, to accelerate sedimentation and in the formation of complexes or to bind water. The host cell can be used as a food. This sequence encodes the A. sydowi fructosyl transferase designated aff-SSY which is described in the method of the invention.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 *GS* sequences given in AAR19001-726837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1b; Page 12-15; 28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene sign ture; messenger
human; clening; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gen · signature HUMGS04398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT22739 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2197 HP; 515 A; 587 C; 575 G; 520 T; 0 other;
                                                                                                                                                                                            Claim 1; Page 1203; 2245pp; Japanese
                                                                                                                                                                                                                                       Identifying gene signatures in 3'-direct for diagnosis of abnormal cell function, reflects relative abundance of corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1996
                                                                                                                                                                                                                                                                                                       WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                    Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              728
                                                                                                                                                                                                                                                                                                                                                                  (OKUH/)
                                                                                                                                                                                                                                                                                                                                                                                  MATES/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                   OKUBO
                                                                                                                                                                                                                                                                                                                                                                                  MATSUBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                    Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                 93,01-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                 94MO-JP01916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA to mRNA; 187 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-biased library; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                          3'-directed human cDNA library function, by preparing cDNA that corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.4;
No. 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relative abundance; frequency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2197;
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                                                                                                                                                                                                                                                                           e.g.
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22223
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    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN90338/c
I/ AAN90338 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 18
                                     Query Match
Best Local
                           Martches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                             The inventors claim an MD probe comprising a purified ss NA:SQ which hybridises to at least a part of the MD gene; pure dystrophin (DS) polypeptide, purified NA encoding DS and antibodies (Ab) to DS. The probes are equal to or greater than 10b of one of 12 cDNA sequences deposited as ATCC 58666-57677. The MD gene is human, or a murine Dmd deposited as ATCC 58666-57677.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of human muscular dystrophy (MD) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 187 BP; 48 A; 42 C; 42 G; 49
                                                                                                                                                                                                                  Muscular dystrophy gene - used for prepn. of probes, dystrophin polypeptide and antibodies for diagnosis and therapy of muscular
                                                                                                                                                                                                                                                    WPI; 1989-220587/30.
P-PSDB; AAP90373.
                                                                                                                                                                                                                                                                                      Kunkel LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dystrophin; muscular dystrophy; probe;
prenatal; heterozygote; gene therapy; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN90338;
                                                                                Sequence 12923 BP;
                                                                                                                                                                                   Disclosure; Fig 5; 68pp; English.
                                                                                                                                                                                                         dystrophy
                                                                                                                                                                                                                                                                                                                                  22-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                       16-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                    W08906286-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foetal screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1992 (first entry)
                                                                                                      gene.
                                                                                                                                                                                                                                                                                                           (CHIL-) CHILDRENS MED CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
                         Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
cagtictcaaaggagcag 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heterozygote; gene reening; ss.
                           Conservative
                                                                                                                                                                                                                                                                                      Monaco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                  87US-0136618
                                                                                                                                                                                                                                                                                                                                                       88WO~US04504
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 209..12923
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                      >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA; 12923 BP
                                                                                 4296 A; 2613 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%;
                                     82.0%;
                                                                                                                                                                                                                                                                                       Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.
Pred. No.
                           0;
                                     Score 16.4;
Pred. No. 1.
                                                                                                                                                                                                                                                                                       ΕP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                            Mismatches
                                                                                  2963 G;
                                                                                                                                                                                                                                                                                      Koenig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ง.8;
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; diagnosis;
                         1.5e+02;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                DB 10;
                                                                                  3044 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                               Length 12923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 187;
                            Indels
                                                                                  7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                            0
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                            0;
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RESULT 9
AAI25968/c
RESULT 10
AAI53359/c
ID AAI533
XX
AC AAI533
XX
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                                                                                                                                                                                                            д
                                                                                                                    Q
                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                             The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                               expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI25968 standard;
          AAI53359;
                                                                                                                                                                                                                                                                                                                                                                                               analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #15901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI25968;
                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 15901; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer;
                                    AAI53359 standard; DNA; 209
                                                                                                                                                                                                            Sequence 209 BP; 47 A; 59 C; 54 G; 49 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                              175 CCGGGTCTCAAAGGAGCAG
                                                                                                            1 ccagttctcaaaggagcag
                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful
zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                           79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11887
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                                                                                                                     19
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                                    89
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                                                                                                                                                 0
                                                                                                                                              Score 15.8; DB 2:
Pred. No. 1.9e+02:
0; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical epithelial cell;
                                                                                                                                                                       22;
                                                                                                                                              Indels
                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                   cells
                                                                                                                                                                         209;
                                                                                                                                                                                                                                                                                                                                                                                                     s ·
                                                                                                                                                 0;
                                                                                                                                                 Gaps
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17-OCT-2001 (first entry)

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RESULT 11
AA116773/c
ID AA116773 standard; D
XX
AC AA116773;
XY
DT 12-OCT-2001 (first
XX
DT 12-OCT-2001 microa
XX
Probe #6706 for gene
XX
Cervical cancer; ss.
XX
PN W0200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89. Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe
                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 22045; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      analyzing
                                                                                                Probe; human; microarray;
cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-)
              30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                   CCGGGTCTCAAAGGAGCAG
                                                                                                                                                                                                                                                            ccagttctcaaaggagcag 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #22045 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single (
                                                                                                                               #6706 for gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                 BP; 47 A; 59 C;
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human;
                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                        79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                                                                                                                                                 563
                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       placenta;
                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon nucleic acid
n human placenta -
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                        Score 15.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                   54 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR
                                                                                                             expression;
                                                                                                                                 analysis in uman cervical cell sample
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                    T; 0 other;
                                                                                                                                                                                                                                                                                             ..9e+02;
2;
                                                                                                                                                                                                                                                                                                                     В
                                                                                                              cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes useful for
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                     209;
                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                 Gaps
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В
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AAI40280/c
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire with continuous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human geno
analyzing
                              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 563
                                                                                                                                                                                                              genetic
                                                                                                                                                                                                                         Probe; microarray;
                                                                                                                                                                                                                                               Probe #8966
                                                                                                                                                                                                                                                                                           AAI40280;
                                                                                                                                                                                                                                                                                                                AAI40280
                                                                                                                      30-JAN-2001;
                                                                                                                                             09-AUG-2001
                                                                                                                                                                  WO200157272-A2
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                     17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 6706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                               used to
                              2000US-0180312
2000US-0207456
2000US-0508408
2000US-0638408
2000US-0632366
2000US-02364587
2000US-0236359
2000US-0236353
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 115 A;
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                       2001WO-US00663
                                                                                                                                                                                                               SS
                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                              measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153
                                                                                                                                                                                                                                                                                                                  563
                                                                                                                                                                                                                                                                                                                                                                         308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487pp; English.
                                                                                                                                                                                                                          placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 178
                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               15.8;
No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                                                                                                                                                                          antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  2.1e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                            diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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5 В

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RESULT 13
AA1486
XX AA1486
XX Probe
DE Probe
KW Probe
KW Geneti
OX Homo s
XX O4-FE
PR 30-JUI
PR 30-JUI
PR 31-SE
PR 04-GC
XX Pen
DX WPI;
XX Human
PT analy
XX The F
CC The I
CC The I
CC The I
CALIBRA AA1486
CC For a c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes analyzing gene expression in human placenta –
                                                                                                                                                                                                                        04-FEB-2000;
-26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #17358 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI48672 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
          The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326
                                                                                                           Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sg,
                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563
                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel
                                                                                       SEQ
                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 115 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No 8966; 654pp; English
                                                                                         No 17358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               to measure
                                                                                                                                                                                                                                                                                                                                                                                                                                          human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.0%;
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                                                                                          654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.8;
pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                               Rank
                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           antenatal diagnosis;
                                                                                                                                                                               DR;
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2.1e+02;
                                                                                                                              probes useful for
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Query Match Best Local S Matches 17

l Similarity 17; Conserv

Conservative

79.0%;

Score 15.8; DB 22 Pred. No. 2.1e+02; 0; Mismatches 2

22;

Length Indels

0

Gaps

0;

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RESULT 14
AAI08987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 564 HP; 137
                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI08987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA108987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #8978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to movel single exon nucleic acid probes. The probes are useful for the present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast particularly those diseases with polygenic aeticlogy. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and processing the processing the present cancer.
                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory
                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2001;
                                                                                                                                                                         Claim 25; SEQ ID NO 8978; (22pp; English
                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                 WPI; 2001-476286/51
                                                      of the breast, fibrocystic non-carcinoma tumours
                                                                                                                                                                                                 in a human breast
                                                                                                                                                                                                         Novel single exon nucleic acid
                                                                                                                                                                                                                                                                           (MOLE-)
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17; Conserv
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2000US-0207456.
2000US-0608408.
2000US-0532366.
2000US-0234687.
2000US-0236359.
1000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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  B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferative breast disease; non-carcinoma tumour.
   A; 149 C;
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Pred. No. 2.1e
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    139 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
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                                                                                                                                                                                                                                                           DK;
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       139 T;
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.1e+02;
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       other;
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172 ccagttcacaaagtagcag 190

ccagttctcaaaggagcag

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AAH00627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic L. acids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (1) CC obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the CC detection of at least one antimicrobial agent resistance gene or at CC ubiquitous detection and for identification of the specific and CC ubiquitous detection and for identification of the specific and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification of series and cc ubiquitous detection and for identification. For a series and cc ubiquitous detection and combine adiacens, Bordeteix against microparation and combine and combin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species specific; genus specific; family specific; probe; detection identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 24; Page 763; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-245006/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Picard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergeron MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; primer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-2000; 2000CA-2307010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2000; 2000WO-CA01150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boissinot M, Huletsky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99CA-2283458
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BP;

210 A;

120 C;

154 G; 189

T; 0 other;

Query Match 79.0%; Best Local Similarity 89.5%; Matches 17; Conservative 0, Score 15.8; DB 22 Pred. No. 2.1e+02; Mismatches DB 22; Indels Length 673; 0

0

В Qy

Search completed: March 4, Job time: 17512 sec 2002, 05:21:23

Mon

OM nucleic .

nucleic search, using sw model

GenCore version $^{4.5}$ Copyright (c) 1993 - 2000 Compugen Ltd.

March 4, 2002, 05:11:29;

Minimum DB s Maximum DB s

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length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*

/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/bcTUS_C.MB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*

Result

Query Match

Length DB

Description Sequence

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8298 12752 12752

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US-08-464-402-1
US-09-054-775C-1
US-09-057-049-1
PCT-US93-03076-1
US-08-459-146-1
US-08-459-065-1
US-09-234-393-5
US-09-234-393-5
US-09-234-393-5
US-09-234-393-5
US-09-234-393-2
US-09-234-393-2
US-09-234-393-2
US-09-258-373-2
US-09-258-373-2
US-09-258-373-2
US-09-258-373-2
US-09-258-373-2
US-09-258-373-3
US-09-258-373-3
US-09-258-373-1
US-08-516-3978-1
US-08-516-3978-1
US-08-053-614-3
US-08-053-614-3
US-09-053-0578-3

Sequence Sequence

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1785 1977 2071 8535 920 1314 1315 2135 2135 2135 2135 2148 3648 3648 3648 3648 3648 3648 4821 4821

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14 15 16 17 18 19 20 20 21 22 23 24 25 25

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

: number of

hits satisfying chosen parameters:

351203 seqs, 113238999 residues

Title: Perfect score:

US-08-956-991-5 20 1 ccagttctcaaagg

ccagttctcaaaggagcagg

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 313, Appli
Sequence 26, Appli
Sequence 49, Appli
Sequence 51, Appli
Sequence 51, Appli
      2 Appli

15, Appl

Appl

17, Appl

1, Appli

3, Appli

3, Appli

3, Appli
                                                                                                                                                                      53, Appl
23, Appl
1, Appli
1, Appli
2, Appli
                                                                                                 TELEFAX: 201-994-1744

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERLSTICS:
LENGTH: 3417 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-464-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-464-402-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08464402 Patent No. 5858705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10T/US95/03939

FILLING DATE: 11 MAK 95

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 35.134

REGISTRATION NUMBER: 35.800-388

REFERENCE/DOCKET NUMBER: 325800-388

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/46
FILING DATE: June 5, 1995
CLASSIFICATION: 435
                               Matches
                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WEI, ET AL.
TITLE OF INVENTION: Hur
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CECCI
STREET: 6 BECKEI
CITY: ROSELAND
STATE: NEW JERSE
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17; Conservative
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US-08-470-260-4
US-08-471-491-4
US-08-477-451-1
US-08-477-451-5
US-08-477-451-5
US-08-477-451-25
US-08-477-451-25
US-08-21-298-40
US-08-21-298-40
US-08-28-255-19
PCT-US95-08565-19
US-08-481-697-410
US-08-850-119-2
US-08-850-119-2
US-08-745-603-1
US-09-461-697-396
US-09-461-697-394
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                                     Score 15.2; D
pred. No. 71;
0; Mismatches
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                                                                       DB 2;
                                                                       Length 3417;
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Sequence
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141, Appl
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11, Appl
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136, Appl
1396, Appl
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US-09-054-775C-1
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                                                                                                                               Sequence 1, Application US/09187049
Patent No. 6117666
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                2559 CCAGTTGTCCAAGGAGAAGG 2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/054,775C FILING DATE: 03-APT-1998 CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/464,402 FILING DATE: 05-JUN-1995 APPLICATION NUMBER: POT/US95/03939 FILING DATE: 31-MAR-1995 ATTORNEY/AGENT INFORMATION: NAME: HOOVER; Kenley K. REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PF161D1
                                                     TITLE OF INVENTION: PLASTID PROTEOLYTIC PROCESSING ENZYME TITLE OF INVENTION: THAT CLEAVES PRECURSOR POLYPEPTIDES
                  NUMBER OF SEQUENCES:
                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     1 ccagttctcaaaggagcagg 20
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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haseltine, William TITLE OF INVENTION: Human DNA Ligase III NUMBER OF SEQUENCES: 10
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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LENGTH: 3417 base pairs
                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                              Lamppa, Gayle K.
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wei, Ying-Fei
  BRINKS HOFER GILSON & LIONE
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85.0%;
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Pred. No. 71;
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; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-09-187-049-1
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FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAILIN, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 321-4200
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9303076
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
TITLE OF INVENTION: GAP-Associated Protein p190 and
TITLE OF INVENTION: Transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local S
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TELEFAX: 312 321-4299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4337 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. B
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2567 CAACTTCTCAAGGGAGCAGG 2586
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia.
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH192-03A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                              COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4337 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                  STREET: 2 Milit:
CITY: Lexington
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                                                                                                                            APPLICATION NUMBER: FILING DATE: 19930:
                                                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                      E: Hamilton, Brook, Smith & Reynolds, P.C
2 Militia Drive
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85.0%;
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pred. No. 74;
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:

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; NAME/KEY:
; LOCATION:
PCT-US93-03076-1
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                        TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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21P: 07110
21P: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Flo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Genetically Engineered Transmissible TITLE OF INVENTION: Hypovirulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 856
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
                             ORIGINAL SOURCE:
ORGANISM: End
ORGANISM: par
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                                                                                                                                                                   MOLECULE TYPE: CI
                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADPLICATION NUMBER: US/08/459,146
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08459146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: George M. Gould, Esq., Hoffmann-La Roche Inc
340 Kingsland Street
EP713
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                                     parasitica)
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                                                           Endothia parasitica (Cryphonectria
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Pred. No. 82;
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US-08-459-065-1
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Patent No. 5882642
Db
                                                                                                                                 STRAIN:
US-08-459-065-1
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Best Local Similarity 85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                            Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12752 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: George M. Gould, Esq., Hoffmann-La Roche Inc
12192 CCAACTCGCAAAGGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER KEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-105/MS-105
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (thoi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically En
TITLE OF INVENTION: Hypovirulence
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROSEMMAN, Catherine R
REGISTRATION NUMBER: 34,240
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (201) 235-6208
                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
STRAIN: EP713
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 8589
                                                                                                                                                                                                                                                           TOPOLOGY:
                1 ccagttctcaaaggagcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                            Conservative
                                                                                                                                                                                                                                                           Linear
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                                                                           76.0%;
85.0%;
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pred. No. 88;
                                                            0;
                                                                           Score 15.2;
Pred. No. 88;
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                                                                                             Length 12752;
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RESULT

GENERAL INFORMATION:

Patent No. 6262333

313, Application US/09328111

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APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
REENT FILING DATE: 1999-06-08
ARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 313
LENGTH: 656
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1)...(656)
; OTHER INFORMATION: n = A,T,C
US-09-328-111-313
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                                                                                         ORGANISM: Abies grandis
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 26, Appli
ent No. 6265639
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Best Local Similarity
                                                                                                                                                                            SEQ IU NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
Query Match
Best Local Similarity
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/234,393A CURRENT FILING DATE: 1999-01-20 EARLIER APPLICATION NUMBER: 60/072,204 EARLIER FILING DATE: 1998-01-22 NUMBER OF SEQ ID NOS: 55 SOFTWARE: Palentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                             APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR113345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                     TYPE: DNA
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                                                                                                                                                       ENGTH:
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88.9%;
      74.0%;
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Pred. No. 85
         Score 14.8;
Pred. No. 97;
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                             DB 4;
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                             Length 1416;
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APPLICANT: Croteau, Rodney H

APPLICANT: Croteau, John E

APPLICANT: Bobliman, Jorg

APPLICANT: Bobliman, Jorg

APPLICANT: Stevele, Keinhard

APPLICANT: Stevele, Christopher L

TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

TITLE OF INVENTION AND METHODS OF USE

FILE REFERENCE: WSUR113345

CURRENT APPLICATION NUMBER: US/09/234,393A

CURRENT APPLICATION NUMBER: 60/072,204

EARLIER APPLICATION NUMBER: 60/072,204

EARLIER FILING DATE: 1998-01-22

NUMBER OF SEQ 1D NOS: 55

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 49

LENGTH: 1785
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; LOCATION: (4)..(1782)
US-09-234-393-49
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                                                                    TITLE OF INVENTION: SESQUITTERPINE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: WSUK13345

CURRENT FILING OATE: 1994-01-20

EARLIER APPLICATION NUMBER: 102/09/234,393A

CURRENT FILING DATE: 1998-01-22

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PALENLIN Ver. 2.0

SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Crock, John E
APPLICANT: Crock, John E
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51, Application #8/05244 030
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                         APPLICANT: Jetter, Reinhard APPLICANT: Steele, Christopher L
                                                                                                                                                                                                                                                                                                              APPLICANT: Bohlman, Jorg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: gamma humulene synthase
            LENGTH: 1785
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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FEATURE:
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Pred. No. 1e+02;
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; NAME/KEY: CDS
; LOCATION: (4)..(1782)
US-09-234-393-51
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Best Local Similarity 88.9%;
Matches 16; Conservative
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APPLICANT: Crotek, John E
APPLICANT: Crotek, John E
APPLICANT: Steele, Christopher L
APPLICANT: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
            GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Crock, John E

APPLICANT: Bohlman, Jorg

APPLICANT: Jetter, Reinhard

APPLICANT: Steele, Christopher L

APPLICANT: Steele, Christopher L

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIK (ABIES GRANDIS)

TITLE OF INVENTION: AND METHODS OF USE
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ratent No. 6265639
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Patent No. 6265639
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OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: gamma humulene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (4)..(1782)
'9-234-393-53
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|1616 agttcttaaayaagcagg 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: PEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: computer-generated nucleic acid sequence encoding OTHER INFORMATION: gamma humulene synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                 REFERENCE: WSUR113345
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Pred. No. 1e+02;
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; NAME/KEY: CDS
; LOCATION: (4)..(1782)
US-09-234-393-23
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US-09-023-023-1/c
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LENGTH: 1977
TOPOLOGY: US-09-023-023-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/U9023023
Patent No. 6121018
GENERAL INFORMATION:
APPLICANT: Kristine Kay Kikly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/234,393A CURRENT FILING DATE: 1999-01-20 EARLIER APPLICATION NUMBER: 60/072,204 EARLIER FILING DATE: 1998-01-22 NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kristine Kay Kikly
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis
RUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Heecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/0 FILING DATE: March 27, It ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READIBLE FORM
                                                                                                                                                          NAME: Han, William T A4,344 REGISTRATION NUMBER: 34,344 REFERENCE/DOCKET NUMBER: GH TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2071 base pairs
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COMPUTER: 1BM COR
OPERATING SYSTEM:
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                                  TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity Matches 16; Conserv

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74.0%;

Score 14.8; DB 3; Pred. No. 1e+02;

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RESULT 14
US-08-716-351A-1
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APPLICANT: Fletcher, Jonathan A.

APPLICANT: Xiao, Sheng
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
TITLE OF INVENTION: HMGI(Y)-LAMA4* FUSION ONCOGENE,
FILE REFERENCE: B0801/7135/ERP
CUBRENT APPLICATION NUMBER: US/09/258,373
CURRENT FILING DATE: 1999-02-26
EARLLER APPLICATION NUMBER: 60/076,401
EARLLER FILING DATE: 1998-02-28
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                RESULT 15
US-09-258-373-2/c
; Sequence 2, Application US/09258373
; Patent No. 6150110
; GENERAL INFORMATION:
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IRAME: BASTIAN, KEVIN L.

REFERENCE_DOCKET NUMBER: 1528

TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08716351A Patent No. 6033905 GENERAL INFORMATION:
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st Local Similarity
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APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
HAME: Bastian,, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1545 AGTGATCAAAGGAGCAGG 1528
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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1977 CAGGTCTCAAAGJGGCAG 1994
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OTHER INFORMATION: /standard_name=
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; SEO ID NO 2
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-258-373-2
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                                            Query Match 72.0
Best Local Similarity 93.0
Matches 15; Conservative
225 TTCTCTAAGGAGCAGG 210
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    HF348620 602019924
AZ297511 RPCI-23-1
AL315219 Tetraodon
BG700618 602662215
BG701055 602662072
BH373590 BH373590
FZ5472 HSD12539 H
BH528026 BH528026
BH367406 BH367406
HB032419 131758 MA
HB044281 HB604281
BH429902 BH429902
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AJ278546 AJ278546	ī	460	84.0	σ	36
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AAGSGGAL VPSSCOSI	10	416	84.0	01	29
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AJZ/04/3 AJZ/04/3	10	401	84.0	٠,	27
AJ2/2002 AJ2/2002	10	388	84.0		26
04025CAV 04026CAV	10	381	84.0		25
NEO2610 AVEO2610	_	373	84.0	٠.	24
Br82665/ CM4-HNUU2		368	84.0		23
BF8.25966 CM4-HNOO2	1	359	84.0		22
2/4	11 BF651521	358	84.0	16.8	21
A1905927 PM-BT103-	0	350	84.0		20
RU5334 YESTCULLI	11	349	84.0		19
A183634U U1-M-AQU-	10	349	84.0		18
AA855923 VW8Ue12.I	10	339	84.0		17
F00929 HS882E032 S	11	338	84.0		16
A1841/2/ U1-M-ALU-	10	334	84.0		15
BB116563 BB116563	10	298	84.0		4
BF825905 CM4-HN002	11 BF825905	292	84.0		13

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/organism="Homo sapiens" /dh_xref="taxon:9606" /dlone="IMAGE:415508" /clone="ib-"KCI_CGAP_Brn67" /tissne_type="anaplastic oligodendroglioma with lp/19q loss"	nttp://image.lini.gov plate: LLMM9426 row: p column: 05 High quality sequence stop: 697. Location/Qualifiers 1 744	Tissue Procurement: David N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the L.M.A.G.E. Consortium/LLNL at:	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Francis: Robert Strausberg, Ph.D.	Eukaryota: Metazoa; Chordata; Craniata; Vertebrada; Eutereocomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 744) NIH-MCC http://mqc.nci.nih.gov/.	RP348620.1 GE:11296215 EST. Homo sapieus	BF348620 744 bp mRNA EST 22-NOV-2000 602019924F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155508 5′, mRNA sequence.

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RPCI-23-117G10.TJ RPCI-23 Mus musculus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                        BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 117 row: G column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Other_GSSs: RPCI-23-117G10.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., dt. Jong, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Clones are derived from the mouse BAC library RPC1-23. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Pieter de Jong
(pieteredejong.med.buffalo.edu). (lones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 838 0200
Fax: 301 838 0208
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/note="Organ: brain; Vector: pCMV-SPORR6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 &b. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 196 c 210 g 150 t
                                                                                                           /note-*Organ: Kidney/Brain: Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoNI and EcoRI Methylase. Size
                  selected DNA was cloned into the pBAC63.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Lite Technologies).

99 c 130 9 94 t
                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-23-117G10"
                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                            /clone_lib="RPCI-23"
/sex="Female"
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                                                                                                                                         CCTGAATGACCTGCAGGAA 87
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Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostel; Neoteleostel;
Actinopterygii; Neopterygii; Teleostei; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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GSS; genome survey sequence.
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19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases. This sequence is a simple read and was generated as part of a large scale clone and sequencing project of the Tetracoon nigroviridis genome. For more intormation, please take a Jook at http://www.accuescope.cms.fr/Tetracodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterization and repeat analysis of the compact genome of the freshwater pufferfish tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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Crollius, H. R., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J., L., L., G., the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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BG700618 559 bp mRNA EST 07-MAY-2001 602682215F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4815146 5', mkNA sequence.
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/db_xref-"taxon:99883"
/clone-"027C17"
                                                                                                                                                                                                                                                                                                                                         /clone_lib-"B"
/note="Genoscope sequence
/note="Genoscope sequence
159 c 176 g 231
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pred. No. 3.5e+02;
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Pred. No. 9.5e+02;
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t 35 others
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 655) NIH-MGC http://mgc.nci.nih.gov/. Mational Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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plate: LLAM10711 row: m column: 03
                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
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cDNA Library Preparation: Michael J.
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mkNA for myosin heavy chain 2b, mkNA sequence.
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1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                               Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                         RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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                                                                                                     Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp, uRL:http://genome.gsc.riken.go.jp/ Carninci.p., Nishiyama,y., Westover,A., Itoh,M., Nagaoka,S., Sasaki Naraninci.p., Nushiyama,y., Westover,A., Itoh,M., Nagaoka,S., Sasaki Naraninci.p., Westover,A., Itoh,M., Nagaoka,S., Sasaki Naraninci.p., Westover,A., Itoh,M., Nagaoka,Y., Maramatsu,M. and Hayashizaki,Y., Sasaki,Y., Sasaki,Y.
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Carrinci, P. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                 HSPD12539 HM3
F25472
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                                                                                                                                                                                                                                                                                       EST
1 (bases 1 to 188)
Lanfranchi,G., Muraro,T., Caldara,F., 'acchioni,B., Pallav
Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
Identification of 4370 expressed sequence tags from a
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                        F25472.1
                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Site_1: Sall; Site_2: HamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
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/clone="C130071C07"
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/strain="C578L/6J"
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90.0%;
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Pred. No. 1.6e+03;
0; Mismatches 2;
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Catarrhini; Hominidae; Homo.
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                                                                     RS Konno, H., Aizwa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukud, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukud, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Mizuno, Y., Nakunura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Watanabe, S., Yamamura, T., Yamanaka, I., T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Kiken Mouse ESTs (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996) 96276048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
18; Conserv
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ABI Chromatograms and other information are available on WWW
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 270)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                      Contact: Yoshihide Hayashizaki
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/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: Not1; The library was constructed by G.
Lantranchi. This library is not subtracted nor normalized.
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/clone- .4000038E11"
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Pred. No. 1.6e+03;
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URL:http://genome.gsc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                      BB367406 274 bp mRNA EST 12-JUL-2000 BB367406 KIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130037M06 3' similar to AB025261 Sus scrofamRNA for myosin heavy chain 2b, mRNA sequence.
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                       house mouse.
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-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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81-45-503-9216
musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared and sequenced in Mc ise Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="n930044H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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/dev_stage="15 days embryo"
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Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, T., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTS (Konno, H., et al.)
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303. 19-44 (1999)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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Laboratory for Genome Exploration Research Group,
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Fax: 81-45-503-9216
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                                                                                     prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                               cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
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18; Conserv
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Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Stone,R.T., Hatton,M.P., Grosse,W.M., Bennett,G.A., Laegrand Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST discovery in swine Unpublished (2000) Contact: Smith TPL
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 64 row: F column: 1
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Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, USA
                                       BB604281 278 bp mRNA
BB604281 RIKEN tull-length enriched, 15 days embryo head Mus
musculus cDNA clone D930013C15 5', mRNA sequence.
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/lab_host="DH10B"
/note="Vector: pCMV SI
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                   .7e+03;
                                                                                                                                                                                                                                              DB 10;
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Sus.
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Query Match
Best Local Similarity
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UKU:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annomated tiltration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carningi, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-44 (1999)
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                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer |5' caracoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronacoronac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Lissue_type-"head"
/dev_stage-"15 days embryo"
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xret "raxon:10090"
/ctone "p930013015"
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                                                                                                                                                                                                                                                                    was cloned into the XhoI and BamHI sites. Vector: modified pBluescript KS(+) after bulk excision from
                                                                                                                                                                                                                                                                                                                                                                               prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain "r57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism "Mus musculus"
                                                                                                                                                                                                                                                                                                                                                  /sex-"mixed"
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                                                                                                                                                                                 . I*
    84.0%;
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    Score 16.8; DB 10;
Pred. No. 1.7e+03;
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                                                 Length 278;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                             source
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BB429902 RIKEN full-length enriched, adult male hippocampus MU
musculus cDNA clone C630030M10 3' similar to M28383 Mouse AE3
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 291)
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The Institute of physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka.S., Sasaki
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka.S., Sasaki
N., Okazaki.Y., Muramatsu,M. and Hayashizaki.Y.
N., Okazaki.Y., Muramatsu,M. and Hayashizaki.Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Kitsunai.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,
Toh,M., Kitsunai.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,
Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu.M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                              19-44 (1999)
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                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="C630030M10"
                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain~"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                             /tissue_type="hippocampus"
/dev_stage="adult"
                                                                                                                                                                                            /clone_lib-"RIKEN full-length enriched,
/note="Site_1: Xho1: Site_2: HamH1; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                        /lab_host-"SOLR"
                                                                                                                                         /sex="male"
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods Enzymol. 303.
                                                                                                                                                                                                              adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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CM4-HN0020-181100-444-d04 HN0020 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwiq.org.br/scripts/gethtml2.pl?tl-CM4&t2-CM4-HN0020-181100-444-d04&t3-2000-11-18$t4-1)
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/note="Organ: head_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini·library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.

Ono, T., Owa, C., Saito, H., Sakai, C., SaLo, K., Shibata, K., Shibata

Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.

Suzuki, H., Tagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.

Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya

T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.

Yano, K., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino

M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Konno, H., et al.)

Unpublished (2000)

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musculus cDNA clone 9530056H01 3' similar to M28383 Mouse AE3 mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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                                                                                                                                                                                                                                                           Automated filtration-based high-thro.ghput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 81-45-503-9216
Email: qenome-res@gsc.riken.qo.jp,
                                                                                                                                                                        further details.
                                                                                                                                                                                                                                        19-44 (1999)
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                                                  /organism="Mus musculus"
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                         /clone-"9530056H01"
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                  FEATURES
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UI-M-A 0-abo-t 04 0-UI.st NIH_HMAP_MCO Mus musculus cDNA clone
UI-M-ALO-abo-t 04-0-UI 4', mkNA sequence.
                                                                         Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized prefrontal cortex library cDNA Library Preparation:

M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996) 97044477
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Fax: 301 443 9890
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Mammalia: Entheria, Rod n. . Schurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, M.F., Lennon, G. and Sodres, M.B.
                                       Seq primer: M13 Forward POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken
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/lab_host.="DH10B"
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Pred. No. 1.7e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/lab_bst="DH10B (Life Technologies)
/lab_pst="Life Library Life Library Life Library Life Library Library
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length: 2000000000
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13 16 16 19	20 20 20 20 20 21 21 21 22 22 22 22 22	22 22 22 20 20 21 19 19
AAH4 8624 AAH4 8625 AAQ20229 AAQ20228 AAQ2028 AAQ80083 AAQ80083 AAQ25979 AAV23650	AAX83631 AAX936463 AAV59705 AAV59705 AAV59705 AAX2570619 AAX24828 AAX24826 AAX	AA136328 AA104749 AAH57390 AAR24616 AAC65855 AAV99703 AAV199704 AAF14961
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ALIGNMENTS

AAV31984 RESULT Synthetic. Homo sapie DS-CAM1; Down syndrome-cell adhesion molecule; neural signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; Human Down syndrome-cell adhesion molecule DS-CAM primer B9-131R. AAV31984 standard; cDNA; 20 BP 28-SEP-1998 (first entry) New isolated hown's Syndrome-cell adhesion molecule - used develop products for detection, diagnosis and therapy of schizencephaly; 23-OCT-1997; 30-APR-1998 WO9817795-A1. WPI; 1998-271791/24. Korenberg JR 25-OCT-1996; (CEDA-) CEDARS SINAI MEDICAL CENT _ sapiens. 96US-0029322 97WO-US19547. diagnosis; assay; human; PCR; primer; SS ť

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reverse primer B9-131R and forward primer B9-131F (see AAV31983) were used in RT-PCR assays of cDNA libraries of various human by tissues to determine human Down syndrome-cell adhesion molecule DS-CAM (see AAV31981 and AAV31988) expression. The results demonstrated expression of human DS-CAM mRNA in foetal and adult brain, and foetal kidney. In addition, a breast carcinoma cell brain, and foetal kidney. In addition, a breast carcinoma cell in the showed expression of human DS-CAM mRNA. DS-CAM polypeptides line showed expression of human DS-CAM mRNA. DS-CAM polypeptides in the developmental and neurological (see AAW42086-87) are associated with developmental and neurological processes. The polypeptides and nucleic acids are used to developmental approducts for the detection, diagnosis and therapy of developmental and neurological approducts for the detection, diagnosis and therapy of developmental approach.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; ds; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DS-CAM1; Nown syndrome-cell adhesion molecule; neural cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV31982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV31982 standard;
        This polynucleotide comprises cDNA tragment E51 that was isolated from a human trisomy 21 foetal brain (14-wk gestation) cDNA library following a modified direct cnNA selection technique applied to bacterial and P1 artificial chromosomes between ETS2 and MX1. E51 was used as a probe to screen the trisomy 21 toetal brain-tibrary. 62 Clones were isolated from the 2 million clones of the original library. Overlapping clones were obtained that were used to deduce a full-length sequence (see AAV31981) coding
                                                                                                                                                                                New isolated town's Syndrome-cell adhesion molecule - used develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
                                                                                                                                                                                                                                                                                 Korenberg
                                                                                                                                                                                                                                                                                                                (CEDA-) CEDARS
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DS-CAMI; bown syndrome cell adhesion molecule: neural signal transduction; trisomy 21; mental retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1998
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holoprosencephaly; corpus callosum agenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331
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This cDNA clone codes for Down syndrome-cell adhesion molecule DS-CAMI (see AAM42086), a cell surface dycoprotein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and plartificial chromosomes between ETS2 and MXI by using cDNA from trisomy 21 human foetal brain. A unique cDNA [cament, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                         New isolated hown's Syndrome-cell adhesion molecule -develop products for detection, diagnosis and therapy developmental and neurological abnormalities
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                                                                                                                                                                                                                 Claim 3; Page 65-72; 109pp; English
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452..521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides are used for inhibiting translation of mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ps-CAM2; nown syndrome-cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; ds; ss.
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                                                                                                    New isolated Down's Syndrome-cell adhesion molecule - used develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
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This cDNA clone codes for bown syndrome-cell adhesion molecule
                                                   Claim 3; Page 83-90; 109pp; English
                                                                                                                                                                                                                    WPI; 1998-271791/24
р-рSDH; ААW42087.
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453..5168
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                                   New isolated hown's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
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Claim 2; Page 81-83; 109pp; English.
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                                                                                                                                                                                                                                                        9608-0029322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1633 A; 1781 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18.4;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1707 G; 1292 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an lecture DS-CAM 3' CONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (14-wk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0;

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Hessully
Anali722
LD Anali722
LD Anali722
LD Anali722
LD Anali XX
XX IAAAI
AC Anali XX
XX Iduma
LE Huma
XX Iduma
KW Iduma
KW Iduma
KW Iduma
KW Iduma
KW Ineur
KW Ineu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc for murine Down syndrome-cell adhesion molecule (DS-CAM), a member of a novel subclass of the 19 superfamily with homology to ce neural cell adhesion molecules. The middle region (see AAV31986) cc neural cell adhesion molecules. The middle region (see AAV31986) cc and 5' region (see AAV31985) of the clone are also provided. The converse of converse 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; CSGP-1; cell surface glycoprotein; CSGP-2; antianemic; nootropic; neuroprotective; anticonvulsant; gene therapy; treatment; diagnosis; hematologic disorder; anemia; myeloproliferative disorder; lymphoma; karyotypic disorder; Klinetelter syndrome: Turner syndrome; peuronal disorder; akathesia; Alzheimer's disease; amnesia; catatonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2173 BP;
                                                                                                                                                                                                         Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUL-2000 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA11722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA11722 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6043056-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epilepsy; neurofibromatosis; ss.
    Polynucleotide encoding
                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ctylatyacctycaggaag 20
|||||||||||||||||
58 ctylatyacctycaagaag 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                            2000-270341/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSGP-2 CDNA
                                                                                     AAW90962
                                                                                                                                                                                                              Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                        9805-0187331
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0187331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "CSGP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              585 A; 598 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%;
94.7%;
                                                                                                                                                                                                              Baughn
        cell surface glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                      MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.4;
Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              554 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                              Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>, -</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                      Guegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>بــ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ammesia; catatomia;
                     is aseful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C
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Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                            diagnosis, treatment and prevention of hematologic disorders such as anemia, myeloproliferative disorders and lymphoma, karyotypic disorders such as Klinefelter syndrome and Turner syndrome, and neuronal disorders such as akalhesia, Alzheimer's disease, amnesia, catatonia, epilepsy and neurofibromatosis. The products of the invention are also useful as probes for mapping the gene sequences encoding CSGP-1 and CSGP-2. This sequence encodes the human CSGP-2 protein described in
                                                                                                                                                                                                                                                                               This invention describes the novel human cell surface glycoproteins CSGP-1 and CSGP-2. The products of the invention have antianomic, nootropic, neuroprotective and anticonvulsant activity and can be used for gene therapy. The encoding nucleic acids are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis, treatment and prevention of hematologic karyotypic disorders and neuronal disorders -
                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                  the
                                                                                            Sequence 1438 BP;
                                                                                                                                  method of the invention.
                                                                                                                                                                                                                                                                                                                                                                             5; Fig 3A-D;
Conservative
                                                                                            355 A;
                                                                                                                                                                                                                                                                                                                                                                               38pp; English.
                    84.0%;
90.0%;
                                                                                              369 C;
  0;
                  Prod. No. 1.5e+02;
    Mismatches
                                                                                              385 G;
                                                                                              329 T; 0 other;
      2
                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
        0;
        Gaps
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x >-- 0.366666666666666666668 x

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AAA96337
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                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; transmymbrane protein; pRO1484; PRO4334; PRO1122; PRO1899; PRO1899; PRO1887; PRO4785; PRO45; PRO4 PRO1889; PRO4387; PRO4785; PRO4787; PRO4
                                                                                                                                                                                                                                                                                                           Schonlein-Menoch purpura; celiae disease; dermatitis herpetiformis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA96337 standard; cDNA;
Homo sapieus
                                                                                                                                                                                                                          Crohns disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA96337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding a novel | Typeptide designated PRO4334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1579 HP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PRO4356;
; PRO6030;
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sig_peptide

84..149 /*Lag.

Location/Qualitiers 84..1406 /*tag- a

WO200056889-A2 28-SEP-2000

01-MAR-2000;

2000WO-US05601.

99US-0125774. 99US-0125778. 99US-0125826.

CDS

23 MAR-1999; 24-MAR-1999; 24-MAR-1999; 31-MAR-1999; 05-APR-1999; 27-APR-1999; 27-APR-1999; 27-APR-1999; 27-APR-1999; 04-MAY-1999;

990S-0127035.
990S-0127706.
990S-0131270.
990S-0131270.
990S-0131272.
990S-0131291.
990S-0132371.

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AA113890
AA113890
AC AA11
XX
AC AA11
XX
DT 12-C
DT 12-C
DT 02-C
DT 09-0
EW Prob
EW Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a secreted or transmembrane polypeptide.

CC The specification describes polypeptides designated PRO/1844, PRO/4334,

CC PRO/182, PRO/1899, PRO/1897, PRO/1857, PRO/4357, PRO/4357, PRO/4405,

CC PRO/182, PRO/1899, PRO/1897, PRO/1895, PRO/1879, PRO/4405,

CC PRO/1826, PRO/1829, PRO/1899, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-1999;
25-MAY-1999;
08-JUN-1999;
20-JUL-1999;
03-AUG-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                   Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                            30-JAN-2001; 2001WO-US00670
                                                                                                                         09-AUG-2001
                                                                                                                                                                                      WO200157278-A2
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                         cervical cancer;
                                                                                                                                                                                                                                                                                                                                         Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI13890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI13890 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue typing
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DB; AAB1891U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cctgaatgacctgcagcaag 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cctgtatgacctgcaggaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                      human; microarray; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eaton DL, Gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe
   2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , प्रम
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0132383.
99US-0135750.
99US-0138166.
99US-0144791.
99US-0146970.
99US-0170262.
                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 A; 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1954 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                   expression analysis in 'uman cervical cell: imple
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Wood WI,
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Pred. No. 1.5e+02;
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Zhang Z;
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RESULT
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Best Local :
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                         04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene sample derived from human cervical epithelial cells. By measuring gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1954 BP; 634 A;
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                                                                                                                                                                                                                     genetic
                                                                                                                                                                                                                                                    Probe #3938 used to measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                AA135252;
                                                                                                                                                                                                                                                                                                                     AAI35252 standard: DNA; 1954
Penn
                   (MOLE-)
                                                    21-SEP-2000;
27-SEP-2000;
                                                                                                                                30-JAN-2001;
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hes 18; Conserv
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SG,
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Hanzel DK,
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2000US-0608408.
2000US-0632366.
2000US-0234687.
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2000US-0608408.
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2000US-0236359.
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                    DYNAMICS
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Chen W,
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Pred. No. 1.5e
0; Mismatches
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 Rank DR
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                                                                                                                                                                                                                                   antenatal
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2;
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cal epithelial cells -
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RRESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ches
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #3744 used
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                                                                                                                                                                                                                                                                                                                                    Penn
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27-SEP-2000;
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                                                                                                                                                                                                                           single exon nucleic human breast .
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18; Conser
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                                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
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2000US-0632366.
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2000US-0236359.
2000US-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312
2000US-0207456
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90.0%;
                                                                                                                                                                                      3744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease; breast cancer; development disorder;
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                                                                                                                                                                                                                                                                                                                                        Chen W,
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nes 2;
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                                                                                                        probe
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
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                                                                               The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a microarray, which can be used for measuring human gene expression in a gample derived from human cervical epithelial cells. By measuring gene
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03-AUG-2000;
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26-MAY-2000;
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                     expression, the probes are therefore useful in grading and/or of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly at ftp.wino.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                        21 - SEP - 2000;
27 - SEP - 2000;
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                                                                                                                                                          Claim
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zing dene expression in homan cervical epithelial cells .
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18; Conser
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                                                                                                                                                                                                                                                                                          20000B - 0234687 .
20000B - 0236359 .
20000B - 0024263 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8P;
                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00670
                                                                                                                                                                                                                                                                                                                                 2000015-0632366
                                                                                                                                                                                                                                                                                                                                                                     200008-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      634 A; 350 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                       I N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8; D
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447
                                                                                                                                                                                                                                              Rank DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysis in human cervical cell sample.
                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                          part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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BP;

714 A;

366 C;

526 G;

349 T;

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δ
                          RESULT 13
AA104749
ID AAI047
                                                                                                                                                                   SXCCCCC
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AAI36328
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× č ×
                                                                                                                 Query Match
Best Local S
Matches 18
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1641 ccagtatgacctgcagaaag 1660
                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #5014 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA136328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI36328 standard; DNA; 1955
                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157272-A2
         AA104749;
                                                                                                                                                                                                                                                                  analyzing
                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                             AAI04749 standard;
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                  Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 cctgtatgacctgcaggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                   SC,
                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid zing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                   1955
                                                                                                                                                                                                                                              SEQ ID No 5014; 654pp; English.
                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  2000018-0180312
                                                                                                                                                                   вР;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to measure gene expression in human placenta sample.
                                                                                                                                                                   714 A;
                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%;
90.0%;
                                                                                                                            84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                              1955
                                                                                                                                                                   366 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                             1660
                                                                                               20
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                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 22;
Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВΡ
                                                                                                                            Score 16.8;
Pred. No. 1
                                                                                                                     Mismatches
                                                                                                                                                                     526 G;
                                                                                                                  1.5e+02;
2;
                                                                                                                                                                     349 T;
                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                            probes useful
                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                     Length 1955;
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                     0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                     0;
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RESULT 1 AAH57390

AAH57390 standard; cDNA; 6016

Вŀ

AAH57390; 10~SEP-2001

(first entry)

skeletal

muscle cell specific cDNA sequence

SEQ

ID NO:230.

Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;

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9
 DЬ
                                                      Matches
                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                     The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing grading, staging, monitoring and prognosing diseases of the human breast, staging, those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe; human; breast disease; breast cancer; development disorder;
inflammatory disease; proliferative breast disease; non-carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04 - OCT - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                          Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn
1641 ccaqtatgacctgcagaaag 1660
                                                                                                                        Sequence 1955 BP; 714 A;
                                                                                                                                              at itp.wipo.int/pub/published_pet_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                     in a
              1 cctutatgacctgcaqqaaq
                                                                                                                                                                                                                                                                                                                                                                                                                                      SG,
                                                                                                                                                                                                                                                                                                                                                                     human breast
                                                                                                                                                                                                                                                                                                                                                                                                             2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                        single exon nucleic
human breast ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #4740 used to measure
                                                                                                                                                                                                                                                                                                                                          25;
                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                          SEQ 1D No 4740;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312
2000US-0207456
                                                                 84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                         366 C; 526 G;
                                                                                                                                                                                                                                                                                                                                                                                acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                        322pp; English.
                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression
                                                      0;
                                                                   Score 16.8; DB 22
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Kank DK;
                                                       Mismatches
                                                                                                                          349 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in human breast sample
                                                                                 22;
                                                         2;
                                                                                 Length
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-carcinoma tumour.
                                                                                                                                                                 part of the printed directly from WIPO
                                                                                     1955;
                                                         0;
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss;
                                                                                                                                                                                                                                                                                        probe
                                                         0
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neuroprotective;

gene therapy; cancer; immunopathology; neuropathology.

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RESULT 1
AAZ24616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 cctyfatyacctycaygaag 20
|||| ||||||||||||||| ||
3100 cctygatyacctycagycag 3119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-2000; 2000WO-US30396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-291057/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY:) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200132927-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sornasse T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6016 BP; 1953 A; 1297 C; 1590 G; 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, immunopathology or neuropathology.
                      17-MAR-1999;
                                                                     23-SEP-1999
                                                                                                                  W09947674-A2
                                                                                                                                                                                                          Human; lung tumor;
                                                                                                                                                                                                                                                         Human lung tumor associated polynucleotide
                                                                                                                                                                                                                                                                                                         07 - DEC - 1999
                                                                                                                                                                                                                                                                                                                                                        AAZ24616;
                                                                                                                                                                                                                                                                                                                                                                                                   AAZ24616 standard; cDNA; 8948 BP
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 158-159; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seithamer JJ,
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0163508
                   99WO-US05798
                                                                                                                                                                                                            lung cancer; T cell stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watson GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 22
Pred. No. 1.6e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>.
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2
                                                                                   Query Match
                                                          Matches
                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1998;
18-MAR-1998;
27-JUL-1998;
27-JUL-1998;
                                                                                                                                                       The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lung cancer. The polypeptides and polypucteotides can be used to stimulate T cells or antigen presenting cells for use in the treatment of lung cancer. The polypeptides and monoclonal antibodies specific for the polypeptides can also be used to inhibit the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
Claim 12; Page 111-114; 148pp; English.
                                                                                                                                                                                                                                                                                                                                  New isolated lund tumor polynucleatides, used to develop products for the treatment, prevention and monitoring the progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-571839/48
                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                Sequence 8948 BP; 2786 A;
                                                                        Local Similarity
                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                              Wand
                                                          Conservative
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98US-0040984.
98US-0123912.
                                                                                                                                                                                                                                                                                                                                                                                                              -<u>-</u>3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9808-0123933.
                                                                       84.0%;
90.0%;
                                                                                                                               2037 C; 2367 G; 1758 T; 0 other;
                                                            <u>..</u>
                                                                        Pred. No.
                                                                                     Score 16.8;
                                                            Mismatches
                                                                        1.7e+02;
                                                                                      DB 20;
                                                                                     Length 8948;
                                                            Indels
                                                            0;
                                                            Gaps
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Search completed: March Job time: 17515 sec 4 2002, 05:21:26

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Run

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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l number of hits satisfying chosen parameters:
 score greater than and is derived by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
08
seq length:
seq length:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-956-991-6
20
1 cctgtatgacctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
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Maximum Match 1008
Listing first 45 summaries
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351203 seqs, 113238999 residues
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-08-998-416-530
US-08-090-523-3
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US-08-398-627-3
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PCT-US93-00321-2
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US-08-464-422-15
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/187,331
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEO ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 1438
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: 2705267 US-09-187-331-4
                                                                                                                                                                                                                                                                   US-08-998-416-530/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
FILE REFERENCE: PF-0631 US
                                                                                                                                                                                                        Sequence 530, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
APPLICANT: Philippsen, Peter
APPLICANT: Politmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
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|| 863 cctgaatgacctgcagcaag
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o. 6043056
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90.0%;
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Pred. No. 17;
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STREET: 3054 Cornwallis Road C17Y: Research Triangle Park STATE: No. 6239264th Carolina

ADDRESSEE:

No. 6239264artis Corporation

COUNTRY:

USA

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Best Local Similarity 89.5%;
Matches 17; Conservative
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INFORMATION FOR SEO ID NO: 530:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 840-base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 98/241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEC. TO.
                                                                                                                                                                                                                                                                                                                                                                              atent No.
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APPLICATION NUMBER: CH 00
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                          APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced Starch Biosynthesis
NUMBER OF SEQUENCES: 51
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Time REGISTRATION NUMBER:
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STRANDEDNESS: singl
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                 CLASSIFICATION:
                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                STREET:
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                                 APPLICATION NUMBER: US
FILING DATE: 19930712
                                                                                                                                                                  ZIP: 63198
                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                               1, Application US/08090523
5. 5498830
                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                              Missouri
                                                                                                                                                                                                                               E: Grace L. Bonner, Monsanto Co. BB4F 700 Chesterfield Parkway No. 5498830th
                                                                                                                                                                                 USA
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 47;
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEPAR: (314) 537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGRAL 1206 NACCONSTRUCT
APPLICATION NUMBER: US 07/539
EILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: BONNEY, GRACE L.
REGISTRATION NUMBER: 38-963
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537.7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-JUN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced Starch Biosynthesis
NUMBER OF SEQUENCES: 51
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bonner, Grace L. REGISTRATION NUMBER: 32,963
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                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/090,523 FILING DATE: 19930712
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                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: St. Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 Chesterfield Parkway No. 5498830th
                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grace L. Bonner, Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1991
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                                                                                                                                 us 07/539763
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                                        38-21(10559)A
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Pred. No. 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Gaps

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US-08-398-627-1
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539763
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,523
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                 TOPOLOGY: 11
MOLECULE TYPE:
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                                   FEATURE:
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STATE: Mis
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STRANDEDNESS: doub
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STREET: 700 Chesterfield Parkway No. 5608149th
NAME/KEY: CDS
LOCATION: 1..1293
                                                                                    STRANDEDNESS: double
                                                                                                                     LENGTH:
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Pred. No. 49;
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RESULT 6
US-08-398-627-3
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US-08-398-627-3
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Best Local Similarity
Matches 17; Conserv
                                                       Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICATION NUMBER: US 08/090,523
APPLICATION NUMBER: US 07/709663
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
PRIOR APPLICATION DATA:
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APPLICANT: Stark, David M.
TITLE OF INVENTION: Enhanced Starch Biosynthesis
NUMBER OF SEQUENCES: 51
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 EILING DATE: 18-JUN-1990 AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                              MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 547-7286
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COMPUTER: 1HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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667 CTCTATGAACTGCTGGAAG 685
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                                                                                                                                                                                                                                          TYPE:
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              2 ctgtaldacctgcagdaad 20
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700 Chesterfield Parkway No. 5608149th
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N: 800
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Pred. No. 49;
                                                                                      Score 15.8;
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US-08-406-858-1
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                                               Sequence 3, Application Patent No. 5648249
GENERAL INFORMATION:
                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 17; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5648249th
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APPLICANT: Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,155
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/US94/05275
FILING DATE: 18 MAY-1994
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
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   APPLICANT:
                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                              Application US/08406858
Barry, Gerard F.
Kishore, Ganesh M.
Stark, David M.
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    Method of improving the Quality of
Stored Potatoes

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89.5%; Pred. No. 49;
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RESULT 9
PCT-US91-04036-1
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Best Local Similarity 89.5%:
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: HHM PC compatible
OPERATING SYSTEM: PC-1005/MS-100S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DAMA:
APPLICATION NUMBER: PCT/US94/05275
FILING DATE: 18-MA: 1994
PRIOR APPLICATION NUMBER: US 08/070,155
FILING DATE: 28-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BONNEY, GRACE L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Bonner, Grace L.
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                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (denomic)
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                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                              APPLICANT: Kishore, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                         667 CTGTATGAACTGCTGGAAG 685
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LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-10S/MS-DOS
                                                                                   COUNTRY:
                                                                                                         STATE:
                                                                                                                        CITY: St. Louis
                                                                                                                                         ADDRESSEE: Monsanto Co.
STREET: 700 Chesterfield Village Parkway
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700 Chesterfield Parkway No. 5648249th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1296 base pairs
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Method of Improving the Quality of Stored Potatoes
                                                                                                                                                                                                              Ganesh M.
Increased Starch Content in Plants
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application PC/TUS9104036 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO:
                                                                                                                      NFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 38-
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTED
OPERATING SYSTEM: PC CONS/MS-DOS
SOFTWARE: Pater.In Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                  REGISTRATION NUMBER: 32706
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7357
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: McBride, Thomas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kishore,
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                       MOLECULE TYPE:
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LOCATION:
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REGISTRATION NUMBER: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: St. Louis
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                                         TOPOLOGY:
                                                         STRANDEDNESS:
NAME/KEY: CDS
                                                                                       LENGTH:
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                                                                       NUCLEIC ACID
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Pred. No. 49;
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PCT-US91-04036-3
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PCT-US94-05275-3
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Best Local Similarity
Matches 17; Conserv
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GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
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COMPUTER READABLE FORM:
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                                                         CURRENT APPLICATION DATA:
                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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PRIOR APPLICATION DATA
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                                                                                                                                                 NUMBER OF SEQUENCES:
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COMPUTER: JHM PC compatible
OPELATING SYSTEM: PC-DUS/MS-DOS
SOFTWARE: Patentin Rel-ase #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/070155
FILING DATE: 28-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
              CLASSIFICATION:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     ENGTH:
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89.5%;
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                                                                                                                                                                  Potatoes
                                                                                                                                                                               Method of Improving the Quality of Stored
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RESULT 13
US-07-735-065-3
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-MAY-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                     TELEFAX: (916) 753-1510 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              FILING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: unassigned
APPLICATION NUMBER: 16-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Glycogen Biosynthetic Enzymes TITLE OF INVENTION: In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Christine K. Shewmaker APPLICANT: David M. Stalker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
TOPOLOGY: 1:
MOLECULE TYPE:
-735-065-3
                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                              REGISTRATION NUMBER:
NAME: Donna E. Scher
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/632,383 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6.0.7 SOFTWARE: Microsoft Word 4.0
                                         STRANDEDNESS:
                                                        TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                            Elizabeth Lassen
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89.5%;
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Pred. No. 49;
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Patent No. 5750875
GENERAL INFORMATION:
APPLICANT: STALKER, DAVID
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                   MOLECULE TYPE: DE HYPOTHETICAL: NO
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APPLICATION NUMBER: 08/016,881
FILING DATE: 11_FEB_1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: GLYCLGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1323 base pair
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 916-753-6413
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NAME: Elizabeth Lassen
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682 CTGTATGAACTGCTGGAAG 700
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NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 6-CLASSIFICATION:
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CITY: DAVIS
                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                          79.0%; Score 15.8;
89.5%; Pred. No. 49;
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Pred. No. 49;
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RESULT 15 US-08-484-434C-13 ; Sequence 13, Apr

Application US/08484434C

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COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LHM PC
OPERATING SYSTEM: Windows NT 4.0; MS Word for Windows 7.0a
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/484,434C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION UNMBER: 08/016,881
FILING DATE: 11-FEB-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Schwedler, Carl J.
REGISTRATION UNMBER: 36,924
REFERENCE/DOCKET NUMBER: 35,924
REFERENCE/DOCKET NUMBER: 31,924
REFERENCE/DOCKET NUMBER: 13:93/01
TELECHONE: 530-792-2463
INFORMATION EFOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13:23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
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; LOCATION: 16..1308
US-08-484-434C-13
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Search completed: March 4, 2002, 05:11:34 Job time: 16948 sec
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GENERAL INFORMATION:
APPLICANT: STALKER, DAVID
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene LLC
STREET: 1920 Fifth Street
                                                                                                                                                                                 Ouery Match 79.0%; Score 15.8; Best Local Similarity 89.5%; Pred. No. 49; tches 17; Conservative 0; Mismatches
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CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: /SIDS2/gcgdata,
3: /SIDS2/gcgdata
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SIDS2/gcgdata/geneseq/geneseqn/Na1980.DAT:*
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SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:*
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HSV L/ST region.
   Sequence encoding P.glumae PG1 lipas
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Human Down syndrom
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cell adhesion molecule n, diagnosis and thera l abnormalities		L CENT.						hown syndrome-cell adhesion molecule; neural transduction; trisomy 21; mental retardation; sencephaly; corpus callosum agenesis; sephaly; diagnosis; assay; mouse; ds; ss.	cell adhesion molecule DS-CAM 5′			2 BP.		ALIGNMENTS	AAV41719 AAX78495	AAV55840	AAHU6555 AAQ20217	AAX56144	AAC66548	AAV48148 AAF97856	AAQ47357	AAZ39519	AAV22674	AAT70227	AAQ87979 AAT96812	AAX16152 AAN91777	AAH06483	AAZ35248	AAX89576 AAZ91408	AAA11992 AA209491	AAI61175	AAT63571	AAA38759 AAA36930	AAA97538
py of								cell;	cDNA.						I-kappa-B-a MAD3 cDNA.	Human Ikappab pory Encodes IkB NF-kap	Sequence of tuf3 g	Human alpha-7 nico	Human kinesin-like Human alpha-7 nico	Human neuroblastom	L5 mycobacteriopha	<pre>LS shuttle phasmid Mycobacteriophage</pre>	DNA sequence of a	Rabbit calcium cha	Rabbit skeletal ca	Rabbit seletal mus	Human cDNA clone (Human BMP-2 gene 5 Micromonospora DNA	Human Ship-2 nucle	Human Ih ion chann	Human polynucleoti	Xylanase gene obta Human breast cance	Human KA-2 recepto	יסי

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic animals, antisense oligonucleotides, and primers useful for amplification of DS-CAM nucleic acids. DS-CAM polypeptides are associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and therapy of developmental and neurological abnormalities such as Down syndrome, mental retardation, holoprosencephaly, agenesis of the corpus callosum, or schizencephaly. Antisense oligonucleotides are used for inhibiting translation of mRNA.
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DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging to a novel subclass of the 19 superfamily with highest homology to neural cell adhesion molecules. A modified direct CDMA selection technique was applied to bacterial and Plartificial chromosomes between ETS2 and MX1 by using CDMA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk gestation) cDNA library. Further clones were obtained by exon trapping, and the complete DS-CAM2 CDNA sequence was identified. DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) and is deleted for the entire transmembrane domain. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome
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                    gestation) CDNA library. Further clones were obtained by exon trapping. The complete DS-CAM1 cDNA sequence was deduced from overlapping clones. A splice variant cDNA (see AAV1988), encoding non-membrane bound DS-CAM2 (see AAV4087), was also identified. Th DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome 21q22.2-22.3. The invention also provides murine DS-CAM partial sequences (see AAV1985-87), expression vectors and host cells, transgenic animals, antisense oligonucleotides, and primers useful for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are associated with developmental and neurological processes. They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1130
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                                                                                                                                                                                                                                                                                                        DS-CAM1 (see AAW42086), a cell surface glycoprotein belonging to a novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA selection technique was applied to bacterial and Pl artificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk
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develop products for detection, diagnosis and therapy
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Pred. No. 1.
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129

Matches Query Match Best Local

Local Similarity

36.5%; 65.1%;

Conservative

0;

Score 307.6; DB 1 Pred. No. 5.6e-79; 0; Mismatches 264

DB 19; 264;

Length Indels

<u>5</u>

Gaps

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This is cDNA clone ethb0018f2. It was isolated from human foetal brain cDNA using a novel method for identifying genes encoding novel secreted or membrane associated proteins. The method involves: (i) liquiting a library of cDNA to DNA such as vector prAP3 (see AV27206) encoding alkaline phosphatase (AP) that lacks signal peptide and membrane anchor sequences (see AAM55047); (ii) transforming bacteria with the products; (iii) transferring, separately, DNA from (some of) the bacterial clones into mammalian cell library that expresses AP; and (v) identifying the corresponding clone in the bacterial library, isolating the mammalian DNA from it and sequencing, ethb0018f2 was characterised mammalian DNA from it and sequencing, ethb0018f2 was characterised as a contains the followed the sequencing ethboring molecule (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal peptide; alkaline phosphatase;
ethb0018f2; ss.
                                                                                                                                                                                                                                                                                by cloning in reporter gene vector without signal sequence transforming bacteria and mammalian cells, and identifying cells that express reporter
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                                                                                                                                                                                                                                                             Claim 8; Fig 5; 50pp; English
                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                       as a partial cDNA clone of a novel neural adhesion molecule (see AAW55045) that contains multiple, consecutive IgG domains. The novel method is very sensitive and is suitable for high throughput
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                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; peripheral nervous system; neuropathy; central nervous system; CNS; alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                             in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Brayer Syndrome. Other uses include the utilisation of the activities such as: Inmune system suppression, Activing activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                           Sequence 5824
                                                                                                                                                                                                                                                                                                                                                                 specification.
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                                             standard;
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2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0653450.

2000US-0652191.

2000US-0693036.

2000US-0727344.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of Herpes simplex virus ICP4 used in the method of the invention as modulators of apoptosis. The method; and products can be used to identify compounds which modulate (stimulate or inhibit) apoptosis in cells. They can be used to immortalise cells for the study of these cells or for growing cells in large numbers for the productions of proteins. They can also be used for stimulating apoptosis in cells, e.g. for treating a subject with a HSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of herpes simplex virus U(s)3 polypeptide - for developing products for modulating apoptosis in cells and for identifying compounds which act as stimulators or inhibitors of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus stimulation; inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Pages 60-63; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ARCH-)
                                                                                                                                                                                                                                                       AAV10362 standard;
                                                                                                                                                                                                                                                                                                                                                                     2169 CCGCGGGGGCTGGCCGGGCCGGGCCAGCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4257 BP; 412 A; 1768 C; 1663 G;
                                                                                                                   Infected
                                                                                                                                                              30-JUN-1998
    Herpes
                                               therapeutics;
                                                                     Infected cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             62 cgctggctcgctggctcqcgggaggccgqgcagcagcagc 101
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    simplex virus
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                                                                                                                                                              (first entry)
                                                    protein number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of the Herpes simplex virus ICP4.
                                                                                                                   protein number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0843659
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/product= "HSV ICP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 361..4257
                                                                                                                                                                                                                                                         cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В;
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                                                                                                                                                                                                                                                           4257
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                                                                            4; ICP4; alpha-4;
                                                                                                                       4 alpha-4 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 T;
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                                                                               cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                               apoptosis;
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        RESULT
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein number 4 (1CP4). Both the alpha-4 gene and ICP4 can be used to block cell apoptosis. Similarly the administration of an agent that inhibits ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells. This can be used for the immortalisation of cells, production of proteins, gene therapy, or inhibition of cell death induced in vivo. They can also be used for production of therapeutics comprising inhibitors of HSV ICP4 function, useful for treating HSV function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09804709-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of herpes simplex virus ICP4 polypeptide - useful for, blocking apoptosis in cells, production of proteins and gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0 other;
                                                                                                     Acrosome reaction protein; P3; sperm protein; polycystin-1; suREJ; Polycystic Kidney Disease and Receptor for Egg Jelly protein; PKDREJ; zona pellucida; fertility; contraceptive; gene therapy; ds.
                                                                                                                                                                                                                  AAZ29335
                 polyA_signa
                                                                                                                                               Human acrosome reaction protein-PKDREJ encoding DNA.
                                                                                                                                                                        29-FEB-2000
                                                                                  Homo
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                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roizman
                                                                                                                                                                      (tirst entry)
/product- "Acrosome re
7636.764]
/*tag- b
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/product= "Infected
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                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    4.78;
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                    Score 39.2; DB
Pred. No. 0.37;
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                            reaction protein (PKDREJ)"
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reaction protein, PKDREJ or P3. PKDREJ is a serm protein involved in binding the sperm to the egg and/or triggerin; the acrosome reaction. It exhibits homology to human polycystin-1 and surke. It can be used to identify antibodies or proteins that block the acrosome reaction and compounds that trigger acrosome reaction in the absence of zona pellucida. Molecules that enhance the efficacy of the acrosome reaction protein can be used to increase fertility and those blocking its action can be used as contraceptives. DNA encoding PKDREJ can be used in gene therapy and also as primer or probe for identifying sequences that encode mutant forms of acrosome reaction protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09964457-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 3; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New functional mammalian acrosome reaction protein, useful for fertility treatment
  misc_RNA
                                                                                                                                                          misc_binding
                                                                                                                                                                                                                                                                                                                                             HSV; junction-spanning transcript; L/ST; therapy; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                HSV L/ST region
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ76213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ76213 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7686 BP; 1952 A; 1827 C; 1809 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDICAL RES COUNCIL.
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                                                                              misc_RNA
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                                                                                                                                                                                                            TATA_signal
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hes 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 cgctggctcgctggctcgcgggaggccgggcagcagcaggggcatgtg 109
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                                                                                                                                                                                                                                                                                           simplex virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                          /*tag= 2
220..225
/*tag= c
/note= "5' end of the L/STs"
370..372
                                                                              /*tag= b
/note= "ICP4 binding
229
                                                                                                                                                                                                               Location/Qualifiers 199..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 12001 BP
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Pred. No. 0.49
0; Mismatches
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                                                                                                          site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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RESULT 10
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An HSV-specific junction-spanning transcript (L/ST) maps at the 5' end to the b repeat sequences of HSV DNA at approx. 3 and 125 kb, and extends into the c repeat sequences of HSV DNA. Compounds that inhibit HSV L/ST synthesis may be used as anti-HSV virucides. The HSV-1 DNA sequence in the region of the L/STs
                                                                                                                                                                                                                                                                                                                                      4505 cngcygggggtygcggggccqygccncggccagccccggg 4544
                                                                                                                                                                                                                                                                                                                                                                                 4445 caggoggggcycytcggcqtucggcggcggcgggggaagcgggggcccgcggggtccctccgg 4504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12001 BP; 1568 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 38-44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes Simplex Virus (HSV) specific junction spanning transcript for inhibiting HSV L/ST synthesis, in the treatment of HSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-022825/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09428156-A
                                                                                                                                                            Sus scrofa domestica.
                                                                                                                                                                                                        Sequence encoding
                                                                                                                                                                                                                              09-APR-1991 (first entry)
                                                                                                                                                                                                                                                        AAN70317;
                                                                                                                                                                                                                                                                             AAN70317 Standard; CDNA; COBB BF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is given in AAQ76213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1993;
                                                                  polyA_signal
                                                                                      mat_peptide
                                                                                                                                                                                  Fertility control; contraception;
           20-MAY-1987
                                 EP222491-A
                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%;
Local Similarity 62.0%;
hes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                              cgctygctcgctqgctcg nyaggccgggcagcagcagg 101
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                                                     /*tag= b
3551..3556
/*tag= c
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/note= "first codon of ORF-1"
                                                                                      /product=hydrophobic signal 958..1307
                                                                                                            /*tag=
                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                         porcine inhibin beta-chain precursor beta-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4557 C; 4315 G; 1561 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39.2; DB Pred. No. 0.6; 0; Mismatches
                                                                                                                                                                                  hormone; spermatogenesis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
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03-OCT-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitorin preproinhibin prodomain intransformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3588
                                                                                                                                                           P.glumae PG1 lipase A gene and stabilisation/translocation function
                                                                                                                                                                                     08-APR-1992
                                                                                                                                                                                                                                     AAQ20372 standard;
                                                                                                                                                                                                                                                                                                                                                1569
                                                                                                  Pseudomomas
                                                                                                                       lipase-specific stabilisation/translocation protein; cleaning system; ORF2; ss.
                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                          2 cgggccgggcucggcggagcgcagcgcaacgcgggggggcgaggccgggcgcgcgtggctcgct
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85US-0783910
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                                                                Location/Qualifiers 483..1559
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                            /*tag= a
/product= lipase_A
1559..2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881 A;
     /label- ORF2
                   /*tag=
                                                                                                                                                                                                                                         DNA; 2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.6%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3588;
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                                                                                                                                               detergent;
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Best Local Similarity
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06-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A P.glumae PGJ genomic library was constructed in cosmid vector c2RB. The lipA gene was isolated by screening with probes based on the vector library and a lipa sequence of the P.glumae librase. Immediately downstream of the lipA yene was found a second open reading frame, designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2. It is ORF2 which encodes the lipase-specific designated ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microorganism for use in detergents - contains lipase gene and a translocation or stabilisation gene, used to produce an efficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-010138/02
P-PSDB; AAR20177, A
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                                        CHC operon; CHC gene cluster; cyclohexanecarboxylic acid; polyketide biosynthetic intermediate; shikimate pathway; shikimic acid-CHC-CoA biosynthetic pathway; doramectin production; recombinant Streptomyces avermitilis bkd mutant; AnsJ/AnsK; AnsL; ChcA; cyclohexenylcarbonyl CoA reductase; AnsM; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1926 egetegatgegetggtgc 1943
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                                                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                                                                      29-JAN-2001
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Streptomyces collinus
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                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 7191
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                                                                                                                                                                                                     collinus CHC (cyclohexanecarboxylic acid) gene operon
                                                                                                                                                                                                                                                        (first entry)
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90EP-0307440
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the CHC (cyclohexanccarboxylic acid) operon of the streptomyces collinus (AAA97538). This operon encodes enzymes involved streptomyces collinus (AAA97538). This operon encodes enzymes involved characteristic pathway: AnsuZA9). In the shikimic acid-CHC-COA biosynthetic pathway: AnsuZA9Ns (AAB23249). Characteristic pathway: AnsuZA9Ns (AAB23251), and ansu (AAB23250). Characteristic pathway: AnsuZA9Ns (AAB23251), and answ (protein sequence not given in the specification). The invention case of the sequence and answ genes, to also relates to the isolated ansuZA9Ns, ansuZ, chcA and answ genes, to callo relates to the isolated ansuZA9Ns, ansuZ, chcA and answ genes, and a grown cassettes comprising at least one of these genes, and a compression cassette. In the host cell comprising such an expression cassette. In the host cell is a bkd mutant of streptomyces avermittilis constitutive erms promoter. This comprision the control of the constitutive erms promoter. This comperon under the control of the constitutive erms promoter the control of the constitutive erms able to produce the comprision of the constitution of the control of the constitution of the control of the con
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P-PSDB; AAB23249, AI
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                                                                                                                                                                                                                                      Corn 1-deoxy-D-xylulose 5-phosphate synthase putative coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7191 BP;
                                                                                                                                   Corn; 1-deoxy-D-xylulose isoprenoid biosynthesis;
                                                                                                                                                                                                                                                                                                                   14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                 AAA38759
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA38759 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5902 ctggcacgagtcgccggtgccgaccgtgcaggcgcaggtgccggcggggac
                                                                         Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggccgcgctggccgtcgccgatgccggtgccyacgccctcgcggtgygtggcgtcgg
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99US-0152930.
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       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA; 698 BP
                                                                                                                                              5-phosphate synthase; herbicide; ss.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a putative coding sequence for the corn 1-deoxy-D-xylulose 5-phosphate synthase enzyme (DXPS). Its protein is 1-deoxy-D-xylulose 5-phosphate synthase enzyme (DXPS). Its protein is 1-nvolved in the isoprenoid biosynthesis pathway. The cDNA was identified by sequencing a number of clones and then comparing their protein to the sequences to known proteins: this showed the sequence's similarity to the capsicum annuum DXPS sequence. The DXPS gene and protein can be used to create transgenic plants which express the gene at either different create transgenic plants which express the gene at either different levels or at different stages of development compared to normal, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide encoding 1-deoxy-D-xylulose 5-phosphate synthase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1998;
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                                                                                       17-JUN-1993
                                                                                                                                            AAQ36930
             Kainate high affinity receptor; EAA2; excitatory amino acid family;
assay; birding affinity; CNS disorders; drugs; ds.
                                                        Human KA-2 receptor gene
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                                                                                                                                                                                                                                                                      ctccgcttgcccgtaalclyqlllalgacgagttlgccgttcttcaccccactagctacc
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                                                                                                                                              standard;
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                                                                                                                                               DNA; 3694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.6; Di
Pred. No. 0.94
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of the gene encoding the human KA-2 receptor, a kainate high affinity receptor of the EAA2 (Excitatory Amino Acid) tamily. The sequence can be used in the identification of sequence related genes. It can also be used to produce calls able to produce the receptor, these cells and membrane fragments of them can be used to assay compounds for binding affinity to human EAA receptor i.e. to screen compounds for potential use as drugs against CNS disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotide encoding human excitatory amino acid-2 receptor - useful for determining binding affinity of cpds. fo the receptor in assaying for drugs to treat CNS disorders
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3694 BP;
                                                                                                                     AAT63571 standard; DNA; 1524 BP
                                                                                                                                                                                2987 GCCGGCACTCCTGGCAGACGCGCACGT 2961
                                                                                                                                                                                                                                3047
                                              xylanase gene obtained by soil DNA amplification.
                                                                        30-JUN-1997
                                                                                               AAT63571;
                        Xylanase; soil DNA;
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                                                                                                                                                                                                                                                                                           2 cgggccgggcycggcggcgcgcgcgagcgcgggqgggcgaggccggcycgtagctcgct 61
                                                                                                                                                                                                                                                                              ctccttyttccagagcttcgcgaatgt 148
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                                                                                                                                                                                                                                             cgctggctcgctggctcgcgggaggcaggcaggaggaggatgtggatactggctct 121
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                                                                         (tirst entry)
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176..229
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230..3115
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176..3118
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Pred. No. 2;
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Best Local Similarity
Matches 76; Conser
                                                                                                                                                                                                                                                A DNA sequence (AAM63571) codes for a novel xylanase (AAW09777). It was isolated from a phagemid in a soil DNA library using as probe a gene fragment (AAM63588) obid. by amplification of soil DNA using degenerate primers (AAM63548-49) based on conserved portions of family F cellulases. It was sequenced by primer walking over the phagemid insert using the same degenerate primers as initial extension primers. Subsequent extension primers were constructed by examining the previously generated sequence data. The novel by examining the previously generated sequence data. The novel by availanase gene can be used for prodn. of xylanase for industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1995;
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                                                                                                                                                                                                             Sequence 1524 BP; 281 A; 537 C; 507
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Carninot, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
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AK015320 G1:12853612
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5hibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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/strain-"C57BL/6J"
                                                                                                                                                            GALTFASKQESGNPTPSGWRIKGQCVATWLSLSASSPLQCRNTLASCLGRKTRSPSLQ
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                                                                                        Mus musculus (strain:c5/81/63) adult male testis clone_lib:RIKEN full-length enriched mouse cDNA l
clone:4921507G06.
                                                                                                                                                                                                                                                                                                                                                             Mus musculus adult
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                                                                                                                                                                                                                                Bukaryota; Metazoa;
                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                      CAP Lidplett.
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                             20499374
             11042159
                                                                                                                               0349636
(bases 1 to 1376)
                                                                                                                (bases 1 to 1376)
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                                                                                                                                                                                                                  Eutheria;
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                                                                                                                                                                                                                                                                                                                                                            male Lestis cDNA, RIKEN tull-length enriched
                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 2.9e-47;
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JOURNAL REFERENCE
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Query Match 27.3%;
Best Local Similarity 67.1%;
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Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
Hanagaki, T., Hara, A., Hayatsu, N., Hiranoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
Imotani, K., Okno, H., Kouda, M., Koya, S., Kurihara, C., Malsuyama, T.,
Kojina, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Malsuyama, T.,
Kojina, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Malsuyama, T.,
Kojina, Y., Kouda, M., Koya, S., Kurihara, C., Malsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K.,
Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Tagama, A., Takahashi, F.,
Sayaki, D., Sibibata, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Tanaka, T., Tejlma, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Tanaka, T., Tejlma, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.,
Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, The Institute of
Interest Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of
Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of
Exploration Research Group, RIKEN Gemomic Sciences Center (Gst),
Rainagawa 230-0045, Japan (E-mail:gemome-res@gsc.riken.go.jp,
Rainagawa 230-0045, Japan (E-mail:gemome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Juli:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second and subsequently enriched for full-length by cap-trapper. Second strand cUNA was prepared with the primer adapter of sequence [5' strand cUNA was prepared with the primer adapter of sequence [5' strand CNA was prepared with Bamil CONA of size comprised longer than 7 kb was with Bamil and Xhol. cDNA of size comprised longer than 7 kb was with Bamil Inost: pnilo Bamil In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yijiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer genome research. 10 (11), 1757-1771 (2000)
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Functional annotation of a full-length mouse characteristics.
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/db_xref="MGD:MGI:1903273"
/db_xref="MGD:MGI:1918065"
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366 c 349 g
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                                                                                                                                                                                                                                                                                                                                                        /clone_lib="kKKEN_full-length_enriched_mouse (DNA_library"
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                           0;
                                                          Score 230; DB 12;
pred. No. 3.1e-47;
                               Mismatches 160;
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Actinopteryali; Neopteryali; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha: Acanthopteryali; Percomorpha; Tetraodontiformes;
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Vector: pBlueScript II KS
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                                                                                                                                                                                                                                                                             Tetraodontidae: Takitudu
1 (bases 1 to 619)
                                                                                                                              One pass dye-terminator sequencing of cosmid cloned genomic
                                                                                                                                                                                                                        Submitted (18-FEB-1997) MRC Human
                                                                                                                                                                                                                                      Direct Submission
                                                                                                                   sequence
                  133
                                                                                                                                                                             phagemid
                             /organism-"Takifuqu rubripes"
/db_xref-"taxon:31033"
/clone_1it-"cosmid 015G16"
/clone="015G16aA10"
                                                                                                     Location/qualifiers
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                    141 g
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                                                                                                                                                                                                             CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
                       156 t
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                         others
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21.0%;

Score 177.2;

DВ

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Length 619;

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2M0212123R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
Clone UUGC2M0212J23 R, DNA sequence.
A.949429
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn,D., Aoyagi,A., Barber,M., Heacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0212 row: J column: 23
Seq primer: CACACGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 616)
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Eukaryota; Metazoa; Chordata; Craniatı; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2949429.1
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                           High quality sequence stop: 616.
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg.,
/lab_host-E. coli strain XL10-Gold, Thresistant, F-m/host-Ecor: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                              /db_xref_"taxon:10090"
/clone="uugc2M0212J23"
/clone_lib="Mouse 10kb plasmid uugc2M library"
                                                                                                                              /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                             Location/Qualifiers
                                                                /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:13820656
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                                                                                                                                                                       AUTHORS
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                                                                                             Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegayo,G., Geer,K., Kroll,M., Shvartsbeyn,A.,
Rossell,D., de Jond,P. and Fraser,C.M.
                                                                                                                                                                                                     вно70312
Unpublished (1999)
Other_GSSs: RPC1-24-257G14.TV
                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                      ви070312.1
                                                                      Mouse BAC End Sequences from Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA se juence.
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pred. No. 4.8e-27;
0; Mismatches 0;
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QY P δÃ

Qy 딛

Locus

VERSION

COMMENT

Tel:

Department of Eukaryotic Genomics The Institute for Genomic Research

9712 Medical Center Dr., Rockville,

MD 20850, USA

Contact: Shaying Zhao

TITLE

FEATURES

Seq primer: SP6 Class: BAC ends.

Location/Qualifiers
1. .710

Clones are derived from the mouse BAC library RPC1-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.clo.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC Resources (http://www.chori.org/bacpac/orderingframe.htm). page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html page: 157 row: G column: 14

end

source

ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
x88325
                                                                                                                                                                                                                                                                                                            Chen,H.M., Rossier,C., Chrast,R. and Antonarakis,S.E. Cloning of trapped exons from human chromosome 21 unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.sapiens DNA
                                                                                                                                                                                                              Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Medical Genetics, University and Cantonal Hospital of Geneva, Medical Geneva, SWITZERLAND
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
3 (bases 1 to 147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSMC18B12
                                                                                                                                                                  Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. ar
Antonarakis, S.E.
Cloning of 559 potential exons of genes of human chromosome
                                                                                                                                                                                                                                                                                 2 (bases 1 to 147)
Antonarakis, S.E.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              X88325.1
                                                                                                                                           exon trapping
Genome Res. 6 (8), 747-760 (1996)
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/clone="RPCI-24-257G14"
/clone_lib="RPCI-24"
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/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note-"Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note-"Vector: pTARBAC1; Site_2: BamH1;
/note-"Vector: pTARBAC1; Site_2: BamH1;
/note-"Spleen' BamH1; Sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:1437728
                                            /chromosome="21"
1. .147
                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                 Location/Qualifiers
                           /note="trapped_exon"
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Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1
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Tetraodontidae: Tetraodon.

1 (bases | to 535)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,

Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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/clone="012c20"
/clone=1ib."G"
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pred No. 9.1e-24;
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Pred. No. 1.9e-21
5; Mismatches 7
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1 (bases 1 to 450)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (DISORDER), Tumor Gene Index (DISORDER)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cyapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                         cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Cione distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 753 Std Error: 0.00
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                                                                                                                                                                                                                                                                                     primer: -40UP from Gibco
                                                                                                                                                                                                                                                                  quality sequence stop: 442.
                74
          /clone="IMAGE:2164965"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Actinopteryqii; Neopreryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
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Tetrandon nigroviridis.
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                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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1 (bases 1 to 1085)
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                         Human gene number estimate provided by genome wide analysis using 
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                          Koest-Crollius,H., Jaillon,O., basilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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Pred. No. 1.6e-17;
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ALZ05171.1 GT:7863990
CSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostei; Actinopterygii; Neopterygii; Teleostei; Inteleostei; Neoteleostei; Actinopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNSU2NAY 1068 bp DNA GSS
Tetraodon nigroviridis genome survey sequence T7
151K15 of library G from Tetraodon nigroviridis,
                                                                                                                                                       Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetracodon nigrovi genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Weissenbach,J.
Charaterization and repeat analysis of the compact
freshwater pufferfish Tetraodon nigroviridis
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1 (bases 1 to 1068)
Roest-Crollius, H., Jaillon, O.,
Bouneau, L., Billault, A., Quetis
                                                                                                                                                                                                                                                                                                               Human gene number estimate
Tetraodon nigroviridis DNA
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                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                 Genoscope.
                                                                                                                                                                                                                                                                                              Unpublished
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/organism-"Tetraodon nigroviridis"
/ob_xref:"taxon:99883"
/clone="035E22"
/clone=1lb="G"
/clone=1lb="G"
/note="Genoscope sequence ID : C08G0
/note="Genoscope sequence ID : C08G0
                    ۵
           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="151K15"
/clone="151E15"
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/note="Genoscope sequence ID : COAG
1 269 c 296 g 257 t 6
                                                                                                                                        Location/Qualifiers
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Quetier,F., Saurin,W., Hernot
                                                                                                                                                                                                                                                                                                                        sequence
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                      ID : COAG151AF08LP1-end
t 6 others
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Tetraodon nigroviridis genome survey sequence T7 end of clone
140F02 of library G from Tetraodon nigroviridis, genomic survey
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Tetraodon nigroviridis.
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Roest-Crollins, H., Jaillon, O., Dasilva, C., Fizames, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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AL198405.1 GI:7836556
                                                                                                                                                                         Direct Submission
Submitted (12-APK-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part o
scale clone-end sequencing project of the Tetraodon nigrov
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 862)
Roest-Crollins, H., Jaillon, O., basilva, C., Boune
Hernot, A., Fizames, C., Wincker, P., Brottier, P.,
Sanrin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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3 (bases 1
                                                                                                                                                                                                                                                                                                                     Tetraodon nigrovinalis DNA sequence
                                                                                                                                                                                                                                                                                                                                      Human gene number estimate provided by genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodontidae;
                                                                                                                                                            http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                (bases 1 to 862)
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                    Ø
         /clone-
/clone_lib="G"
/note="Genoscope sequence
/note="Genoscope sequence
                                                                 /organism-"Tetraodon nigroviridis"
/db_xref-"taxon:99883"
/clone-"140F02"
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Pred. No. 5.4e-11;
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                        COAG140DC01LP1~end 23 others
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Query Match Best Local Similarity

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Score 78.8; DB 13; Pred. No. 2.3e-09;

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AL191311
AL191311.1 G1:7829415
AL191311.1 G1:7829415
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
                               CNSO2CLY 611 bp DNA GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence pUC-Ori end of clone 255N21 of library G from Tetraodon nigroviridis, genomic survey
gtgtttgcaagcacateggggacyctggtgccctgcccqqctgcaggcatccctqtq-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodontidae; Tetraodon.

1 (bases 1 to 611)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizanes, C., Fisher, C. Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryot: Metazoa; Chordata; Cranial: Vertebiata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                              102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius, H., Jaillon, O., Dasi
Bernot, A., Fizames, C., Wincker, P.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                              Submitted (12-APR-2000) to the EMBL/GenHank/DDBJ databases this sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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3 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene number estimate provided by genome wide analysis using
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                                                                                              Conservative
                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="255N21"
/clone=1ib="6"
/note="Genoscope sequence ID : COAG255CG11SP1-end
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pred. No. 5.7e-07;
5; Mismatches 43; Indels
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p., Brottler,P., Quetler,F.,
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Tetraodontidae; Tetraodon.

(bases 1 to 656)

Roest-Crollius,H., Jaillou,O., Dasilva,C., Fizames,C., Fisher,C.,

Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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Human gene number estimate provided by genome wide Tetracodon nigroviridis DNA sequence Unpublished 3 (bases 1 to 656)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission submitted (12-Apk 2000) to the EMBL/GenBank/DDBJ databases submitted (12-Apk 2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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sequence.

AL292982.1 GI:8031562
GSS; genome survey sequence.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

TE 1 (bases 1 to 691)
Bouneau,I., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
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blobelgeNgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
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ALO27078.1 G1:326421
ALO27078.1 G1:326421
GSS; genome survey sequence.
GSS; genome survey sequence.
Takifugu rubripes
Takifugu Teleostel; Butelcostel; Neotelcostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Telraodontiformes;
Acanthomorpha; Acanthopterygii; Percomorpha; Telraodontiformes;
Takifugu
Telraodontidae; Takifugu
Telgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
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/clone="13 g 111 t
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/db_xref-"taxon:31033"
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Search completed: March 4, Job time: 6499 sec

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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                          rnis sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.denostope.chs.fr/Tetraodon.
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/db_xref-"taxon:99883"
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Best Local Similarity 65.1%;
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                                                                                                                                   GENERAL INFORMATION:
                                                                 APPLICANT: Leopardi, Rosario
APPLICANT: Rolizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES: 2
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CORRESPONDENCE ADDRESS:
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STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
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                                                                                                                                                                                                                                      792 ggtttgaccaccgccaaaccatggccgggcac-gcgtggagctgccttgc 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCCCCCAGCGCCCTTCGATGGTACCTGGCCACAGGGGACGACATCTACGACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcatccctcctgtgactctcagatggtacctagcaacgggcgaggagatctacgatgtcc 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaattagaagtcaggatgtccacatcaaggctgttttacgggagccctatacagtccgtg 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCACATCCGGCACGTCCACGCCAACGGGACGCTGCAGCTCTACCCCTTCTGCCCCTCCG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cogggatcogcoacgtocoatcocoaatggcoactotocoaaattttococotttocottoaa 372
                                                                                                                                                                                                                                                                                                                                                                                                                              gcaactgcgcgagactgttcgtgtcagaaccagcaaactc-agcccatccatcctggaag
                                                                                                                                                                                                                                                                                                                            ACCCCCTCTCCACCTATCGCTGCATCACCAAGCACAAGTATAGCGGGGGAUACCCGGCAGA
                                                                                                                                                                                                                                                                                                                                         atgggctgtacaactaccgctgcatcgcgcggcacagattcgcgggggggagacgagacaga 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATCCGGAGCCCCAACATCCGCGTCAAAGCAGTTTTCAGGGAACCCCTACACCGTCCGGG
                                                                                                                                                                                                                                                                           GCAATGGGGCACGCCTCTCTGTGACAGACCCTGCTGAGTCGATCCCCACCATCCTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 307.6; DB 2; pred. No. 1.7e-82; 0; Mismatches 264;
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US-09-259-821A-1/c
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                                                                                                                                                                                           ; TYPE: DNA ; ORGANISM: HERPES VIRUS, TYPE 1 US-09-259-821A-1
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Best Local Similarity 62.0%;
Matches 62; Conservative
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: 185/09/259,821A
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEO 1D NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 1
LENGTH: 4257
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09259821A
Patent No. 6210926
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleic acid
                                                                                                                    Matches
                                                                                                                                   Query Match

Best Local Similarity 62.0%;
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEOPARDI, ROSARIO
APPLICANT: KOIZMAN, HERINGRU
TITLE OF INVENTION: HERIPES SIMPLEX VIKUS ICP4 1S
                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08
FILING DATE: 26-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARTELECOMMUNICATION INFORMATION:
TELEPHONE: 512,418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2229 CAGGCCTOGCCCTCGCCCTCCGGCGGCGCGGGGGAAGCGGGGGCCCGCGGGTCCCTCCGG 2170
2169 CCGCGGGGGCTGGCGGGCCGGGCCAGCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                        Highlander, Steven L
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                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                              ARCD: 317
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                                                                                                                      Score 39.2; DB Pred. No. 0.066; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.2; DB pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                      DB 4;
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        2130
                                                                                                                                                                                                                                                                                                                                                                                 AN INHIBITOR OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4257;
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US-08-843-659-1/c

Patent No. 6218103

GENERAL INFORMATION:

APPLICANT: Leopardi,
APPLICANT: Roizman,
TITLE OF INVENTION:
TITLE OF INVENTION:

Bernard Roasrio

HERPES SIMPLEX VIKUS US3 AND ICP4 AS INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

E: Arnold, White & Durkee p.O. Box 4433

Sequence 1, Application US/08843659

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ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type 1
US-08-458-568A-11
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Sequence 32, Application US/UB197792
Patent No. 5525488
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (215) 568-34
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30.317
REFERENCE/DOCKET NUMBER: DFF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
SOFTWARE: patin (Genericech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,792
FILING DATE: 16-FEB-1994
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-1015/MS-DOS
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                               STREET: 460 FOREST STREET: 460 FOREST STATE: California
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                                                                                                                                ZIP: 94080
                                                                                                                                              COUNTRY:
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460 Point San Bruno Blvd
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pred. No. 0.11;
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TOPOLOGY: US-08-843-659-1

STRANDEDNESS:

nucleic acid EDNESS: single

linear

TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs

ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642

CLASSIFICATION:

APPLICATION NUMBER: US/08/843,659

Concurrently Herewith

REFERENCE/DOCKET NUMBER: ARSB:519

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURKENT APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY: U ZIP: 77210

CITY: Houston ADDRESSEE:

Texas

United States

ξ Ş RESULT 5 US-08-458-568A-11 5 Query Match Best Local Similarity Sequence 11, Application US/08458568A Patent No. 5821339 Matches GENERAL INFORMATION: APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: 2169 ссасвававствосовыйстваесссийсськогосовы 2130 STREET: One Liberty CITY: Philadelphia STATE: PA ADDRESSEE: 62; E: Woodcock, Washburn, Kurtz, Mackiewicz & No. One Liberty Place, 46th floor Conservative 4.7%; 62.0%; Compositions and Methods for Treatment of Herpesvirus 0; Mismatches Score 39.2; DB 4; Length 4257; pred. No. 0.066; . 8 Indels 5821339ris 0 Gaps 0

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 08-OCT-1

08-OCT-1992

07/958414

PRIOR APPLICATION DATA:

07/744207

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                                                                                                                                                                                                                                                   Sequence 32, APF--
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Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION UNMBER: 05-7UL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/9067
FILING DATE: 31-DFC-1007
PRIOR APPLICATION
                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
APPLICATION NUMBER: 05/783910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E
REGISTRAFION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  1569 TCCTTTCTTCCTCCAGCATCGGAGTGGGGACAGCAGTTGCTCCAACGGGAATATTGTCCT 1628
                                STATE: COUNTRY: 21P: 940
                                                                                                                                                                        APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
                                                                                                                                                                                                                                                                                                                                                        1629 CTCCTTT 1636
                                                                                                                                          TITLE OF INVENTION: Using such Nucleic Acid NUMBER OF SEQUENCES: 44
COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                   122 ctccttgt 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: singl
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TELEX: 910/371-7168
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                                                                           ADDRESSEE:
STREET: 46
CITY: Sout
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                                94080
                                                           South San Francisco
: California
                                                                                                                                                                                                                                                                      Application US/08459850
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                                                                                               460 Point San Bruno Blvd
                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                Genentech,
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Sequence 32, Application US/08459214
Patent No. 5716810
Patent No. 5716810
Patent No. 5716810
PappLICANT: Peter H. Seeburg
APPLICANT: Peter H. Seeburg
ITITLE OF INVENTION: Nucleic Acid Entitle OF INVENTION: Beta Chains of TITLE OF INVENTION: Using such Nucleic Number OF Sequences: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: US-08-459-850-32
                                                                                                                                                               US-08-459-214-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 12-AUG-
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APPLICATION NUMBER: (
FILING DATE: 03-OCT-1
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APPLICATION NUMBER: (
FILING DATE: 07-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              1509 CGGWYTY CGGGGGGGGGGGGACGACCCT 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/459,850 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                        1569 TCCTTTCTTCCTCCAGCATCGGAGTGGGGACAGCAGTTGCTCCAACGGGAATATTGTCCT 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/1 FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                     1629 CTCCTTTF 1636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 31-DE
                                                                                                                                                                                                                                                                      122 ctccttgt 129
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Local Similarity 56.28;
nes 72; Conservativo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       62 cgctyyctryctyyctcycygaagycaycagcagggycalgtggatactggctct 121
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SYSTEM: PC-DOS/MS-DOS
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       Seeburg
Nucleic Acid Encoding the Alpha or
Heta Chains of Inhibin and Method for Synthesizing Polypept
Using such Nucleic Acid
44
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CORRESPONDENCE ADDRESS:

Genentech,

ADDRESSEE: STREET: 40 CITY: Sout

south San Francisco

California

USA

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE: 17-FEBPRIOR APPLICATION DATA:

17-FEB-1994

08/197792

PRIOR APPLICATION: 435

APPLICATION NUMBER: US/08/459,214 FILING DATE: 02-JUN-1995

APPLICATION NUMBER: 07/958414

PAPPLICATION UNTER: 08-0CT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744207

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988

FILING DATE:

APPLICATION NUMBER: 07//-FILING DATE: 12-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-DEC-

31-DEC-1986

06/906729

PRIOR APPLICATION DATA:

06/827710

PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

03-OCT-1985 07-FEB-1986

06/783910

APPLICATION NUMBER: FILING DATE: 07-FEB

COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,

360 Kb floppy disk

94080

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; NAME/KEY:
US-08-716-942-24
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APPLICANT:
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Best Local Similarity 54.2%;

Matches 77; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Marina I. Larson
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                       ORGANISM:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: genomic DNA
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                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/716,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/004,157 FILING DATE: 20-Sep-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                        TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                   121 teteettettecagagettege 142
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                                               212
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  272
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5849491
                                                                GCCAGCAGTTCGACATGGTCAC 293
                                           ACTTEGUGACTGAGGTCACCGGGAACATGATCAACAACTCGACGATCACGAACCTGGCAG 271
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                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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Radomski, Christopher C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yap, Wai Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warren, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                  sequence of xylanase gene identified by amplification of xylanase fragments from
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                                                                                                                                                                                                                                                                                                                                        double
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SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
COMPOSITIONS OBTAINED THEREBY
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                                                                                                                                                           Score 38; DB 2;
pred. No. 0.09;
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                                                                                                                                                 Mismatches
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                                                                                                          211
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TOPOLOGY: US-08-459-214-32

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

TELEX: 910/371-7168
NEORMATION FOR SEQ ID NO:

910/371-7168

415/952-9881

TELEFAX:

SEQUENCE CHARACTERISTICS:

3588 bases

LENGTH:

REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896 ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616

REGISTRATION NUMBER:

297P2D6

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2 cgggccgggcycyqcggagcgcaqcgcaacqcgqggyqcyaggccgggcqcgtygctcgct 61

1569 TCCTTTCTTCCTCCAGCATCGGAGTGGGGACAGCAGTTGCTCCAACGGGAATATTGTCCT 1628

62 cgctqqctcgctggctogcgggaggccgqgcagcaggaggatgtqalactggctct 121

Matches Query Match

Local Similarity 56.2 nes 72; Conservative

4.6%;

Score 38.4; DB 1; pred. No. 0.11; Mismatches

Length 3588; Indels

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Gaps

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122 ctccttgt 129

RESULT 9 US-08-716-942-24

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                                                                                                                                                                                                                        Query Match 4.5%;
Best Local Similarity 49.5%;
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                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETFROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                       1746
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                                                                                              1806
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                                        1866
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]31 ttgtcaatgcatcgctgc 198
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doub
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REGISTRATION NUMBER:
                                                                                                                           61
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TELEX: 6714627 CUSH
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                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                      9,
                                          tctccttqttccagagcttcgcgaatgttttcagtgaagagccccactccagcctctact 180
                                                                                                TGGCTGGCTCGCATGCGCGCGCGCTGCCGCTGGCCGGCGGCGGCGCGCTCGCGACGACGC
                                                                                                               CCGCGGCAAGCGGCGCGGGGGGGCGCCATGCCGTTGCCG, JCGGCGCTGCCGGGCGCGC 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOS, Jannetje W
                                                                                                                                                                                                             Conservative
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483..1556
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Pred. No. 0.12;
                                                                                                                                                                                                                Mismatches
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US-08-449-015-9
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                                                                                                                                                                                                        Matches
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Best Local Similarity 49.5%;
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TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FRENKEN, León G.
APPLICANT: VERKLPS, Cornells T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKUlis, Paul N.
REGISTRATION NUMHER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                      1806
                                                                                                                                   1746 ССОСИОСЛАССИИСИСИИСИИ ОВИСОВИТЕЛЕНИЯ ТОССОВСЕССТВОССОВСЕССЕ 1805
                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-10S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1615 L.: CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 24-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                     | 121 totoottigittocagagottogogaatgttttoggtgaagagococcactocagoctotact 180
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                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                      NAME/KEY:
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Pred. No. 0.12;
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TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
CURRENT FILING DATE: 1998-01-27
RARLIER APPLICATION NUMBER: 60/035,963
FARLIER FILING DATE: 1997-01-27
ARLIER FILING DATE: 1997-11-06
NUMBER OF SE0 ID NOS: 33
SOFTWARE: FBStSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
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US-09-244-796-17/c
: Sequence 17, Application US/09244796
: Patent No. 6281344
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Best Local S
Matches 23
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Patent No. 6258558
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APPLICANT: Roberts, F
APPLICANT: Liu, Rihe
               GENERAL INFORMATION:
APPLICANT: SZOSEAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
-09-007-005-17
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REFERENCE:
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 00786/350007
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9.3%; Pred. No. 0.089;
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                                         RNA-PROTEIN
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; NAME/KEY: misc_feature
; LCGTION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or
US-09-244-796-17
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US-08-091-569-1/c
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08091569 Patent No. 5494792
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Translation template
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                APPLICANT: KAMBOJ, Rajender
APPLICANT: NUTT, Stephen
APPLICANT: SHEKTER, Lee
APPLICANT: WOSNICK, Michael
TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS
TITLE OF INVENTION: THE HAA2 FAMILY
                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 gccccactccagcctclactttgtcaatgcatcgctgcaagaggtagtgtttgcaagcac
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                                                                                                                                COUNTRY:
                                                                                                                ZIP:
                                                                                                                                                      STATE:
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                                                                                                                  22313-0299
                                                                                                                                                      Virginia
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                                                                                                                                                                                              Suite 500
                        Version #1.25
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PRIOR APPLICATION DATA:

FILING DATE: CLASSIFICATION:

APPLICATION NUMBER:

US/08/091,569

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Best Local Similarity 53.1%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08203676 Patent No. 5614406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/750,081
FILLING DATE: 27-AUG 1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3047 CGGGGACGCCCACGCCGACGCCGGAGGCCCCCCACGCCCCCACGCCCCTGGATGC 2988
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TELEFAX: 899149
                                                                                                                                                                                            APPLICANT: KAMBOJ, Rajender
APPLICANT: NUTT, Stephen
APPLICANT: SHEKTEK, Lee
APPLICANT: WGSNICK, Michael
TITLE OF INVENTION: KAINATE-BINDING HUMAN CNS RECEPTORS
TITLE OF INVENTION: THE EAA2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                            2987 GCCGGCACTCCTGGCAGACGCGCACGT 2961
COMPUTER READABLE FORM:
,MEDIUM TYPE: Floppy disk
,COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             122 ctccttgttccagagcttcgcgaatgt 148
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STRANDEDNESS: double
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                                                                                               STREET: 1800 Diag
CITY: Alexandria
STATE: Virginia
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                                                                 COUNTRY: USA
ZIP: 22313-0299
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                                                                                                                                 1800 Diagonal Road,
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176..3118
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Search completed: March 4, 2002, 05:12:23 Job time: 16997 sec
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Best Local Similarity 53.1%;
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INFORMATION FOR SEO 10 NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/7:
FILING DATE: 27-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 24,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/203,676
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TELEPHONE: (703)683-4109
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TYPE: nucleic acid
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SOURCE KEYWORDS VERSION DEFINITION REFERENCE ACCESSION Locus COMMENT TITLE JOURNAL AUTHORS New J. (Losses L.C. 27)

PRS (Ronno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci Fonno, H., Aizawa, K., Kayawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakanura, M., Oda, H., Okazaki, Y., Matsuyama, T., Shinada, Y., Shipata, Y., Shigemoto, Y., Shinadaya, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Y., Shigemoto, Y., Shinadaya, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, A., Watanabe, S., Yamamura, T., Yamanaka, I., T., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
La Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN) BB336040 279 bp mRNA EST 11-JUL-2000 BB336040 RIKEN full-length enriched, 10 days neonate medulla bB336040 RIKEN full-length enriched, 10 days neonate medulla oblongata Mus musculus cDNA clone B830046F24 3′ similar to AF217525 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule (DSCAM) mRNA, mRNA sequence. Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 279) Mus musculus EST BB336040.1 G1:9044803 вн 336040 house mouse Chordata: Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus.

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Carninci.p., Nishiyama,Y., Westover,A., Itoli,M., Nagaoka,S., Sasaki
Carninci.p., Nishiyama,Y., Westover,A., Itoli,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y., and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)

System. Genome Res. 9 (5), 463-470 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization cap-trapper. cDNA went through one round of normalization to Rot - 20.0 and subtraction to Rot - 459.0. Second to Rot - 20.0 and subtraction to Rot - 459.0. Second to Rot - 20.0 and subtraction to Rot - 459.0. Second strand cDNA was prepared with the primer adapter of strand cDNA was prepared with XHoI and BamHI. Vector: a 3/1 cDNA was cleaved with XHoI and BamHI. Vector: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="medulla oblongata"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/note="Site_1: Sal1: Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:100
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Laboratora Yano, K., Yasunishida Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap Tel: 81-45-503-9222
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URL:http://genome.qsc.riken.go.jp/
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                                                                                                                                       Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci S., Fukunda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Itoh, M., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kaqawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakanura, M., Oha, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shiyama, A., Shiraki, T., Suyabe, Y., Suyahara, Y., Suzuki, H., Tayawa, A., Shiraki, T., Suyabe, Y., Suyahara, Y., T., Tsunoda, Y., Watahiki, A., Watahabe, S., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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1 (bases 1 to 252)
Sciences Center(GSC), Yokohama Institute
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                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
tohA. Proc. Natl. Arad. Sci. U.S.A. 95 (2), 520-524 (1998)
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Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Site_1: Sall: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Genome Science Experimental Animal Research in Riken Riken Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer (5^\prime)
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/lab_host="pH10B"
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/clone="C230015109"
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RESULT 4
BB336019/c
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Al Unpublished (2000)

Al Contact: Yoshihde Hayashizaki
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BB336019 RIKEN full-length enriched, 10 days neonate medulla
oblongata Mus musculus cDNA clone B830046C02 3' similar to AF217525
Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., WesLover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishiyama,Y., WesLover,A., Itoh,M., Nagaoka,S., Sasaki
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Carninci, p. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                          Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
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/note="Site_1: Sal1; Site_2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia prepared and sequenced in Mouse Genome Encyclopedia prepared and sequenced in Mouse Genome Encyclopedia
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/tissue_type="medulla oblongata"
/dev_stage="10 days neonate"
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                              /clone="B830046C02"
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RESULT 5
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Mammalia: Entheria: Rodentia: Schrödnathi: Muridae: Murinae: Mus
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                      Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.go.jp.

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Thermostabilization and thermoactivation of thermolabile enzymes by trohalose and its application for the synthesis of full length trohalose and its application for the synthesis of full length cona. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) cona. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carningi,P. and Hayashizaki,Y...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Genomic Sciences Center and Genome Science Laboratory in Genomic Science Experimental Animal Research in Riken RIKEN Division of Experimental Animal Research in Riken
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Mus musculus cDNA clone D130072G13 3′ similar to AF217525 Homo
sapiens clone cDSC1 DOWN syndrome cell adhesion molecule (DSCAM)
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UKU:http://denome-reseasc.riken.go.jp/
Carninci.P., Nishiyama.y., Westover.A., Itoh,M., Nagaoka,S., Sasaki
Carninci.P., Nishiyama.y., Westover.A., Itoh,M., Sasaki
y., N., Okazaki.y., Muramatsu,M. and Hayashizaki.y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
TOmaru,Y., Carninci.P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Tomaru,Y., Carninci.P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(CSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suethiro cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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1. Konno, H. Aizawa, K. Akahira, S., Akiyama, J., Arakawa, T., Carninci R. Konno, H. Aizawa, K. Akahira, S., Akiyama, J., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., P., Endo, T., Kori, L., Ishik, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kaj, C., Kawai, J., Kikuchi, N., Izawa, M., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Shibata, K., Saito, K., Shibata, K., Shibata, K., Saito, H., Sato, K., Shibata, K., Sogabe, Y., Sugahiara, Y., Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahiara, Y., Y., Shinagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominada, N., Toya, N., Yasunishi, A., Yoshida, K., Yoshida, K., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y., Shinashi, S., Saito, K., Shibata, Y., Nakamura, Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y., Rikin Mouse, EsTs. (Konno, H., et al.)
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Yoshihide Hayashizaki
Email: genome-res@gsc.riken.qo.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S.,,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Pred. No. 1.1e-49;
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Carninci, P., and Hayashizaki Y. Carninci, P., and P., and Hayashizaki Y. Carninci, P., and P., and Hayashizaki Y. Carninci, P., and P.
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BB329941 248 bp mRNA
BB329941 RIKEN full-length enriched, 6
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/db_xref="taxon:10090"
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/dev_stage="6 days neonate"
/lab_host="bH10H"
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/clone_lib="RIKEN_full-length enriched, 6 days neonate
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         EST 11-JUL-2000 days neonate medulla
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Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 248)
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Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-resegsc.riken.go.jp,
URU:http://genome.gsc.riken.go.jp/
URU:http://genome.gsc.riken.go.jp/
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
N., Okazaki,Y., Muramatsu,M. Sasaki
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of the so, thesis of full length
trephalose and its application for the so, thesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Tohan,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tohan,M., Carninci, P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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The Institute of Physical and Chemical Research (RIFEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa (0-0045, Jap
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details
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                                                                                                                                                                                       /clone="B730003122" /clone_lib="RIKEN full-length enriched, 6 days neonate medulla oblongata"
/tissue_type="medulla oblongata"
/dev_stage="6 days neonate"
/lab_host="DH10B"
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Al. Unpublished (2000)

Al. Contact: Yoshihide Hayashizaki
A., Yokohama Institute
Scilences Center (GSC), Yokohama Institute
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BB330426.1
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSCAM) mRNA, mRNA sequence.
                                                                                                                                   Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                            Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
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ILOh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
TOMATU,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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                          BB331552 253 bp mRNA EST TOLL FOR BB331552 RIKEN full-length enriched, 6 days neonate medula BB331552 RIKEN full-length enriched, 6 days neonate medula oblongata Mus musculus cDNA clone B730035G02 3′ similar to AF217525 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule (DSCAM) mRNA, mRNA sequence.
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 81-45-503-9222
Fax: 81-45-503-9216
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P. Endo, T. Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Itazawa, M., Kadola, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Nakamura, M., Oda, H., Oho, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata (Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shiqamato, Y., Shiqamato, Y., Shiqamoto, Y., Shinadawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Y., Shiqamoto, Y., Matanaba, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
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URL:http://genome.qsc.riken.go.jp/
Carninci.p. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci.p. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okozaki,Y., Muramatsu,M. and Hayashizaki.Y.
N., Okozaki,Y., Muramatsu,M. and Hayashizaki.Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), S20-524 (1998)
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y., and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
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Contact: Yoshihide Hayashizaki
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
GAGAGAGAGAAGAGGCTCTTTTTTTTTTTTTTTTTTVN 3'], CDNA was prepared by using trebalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second
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                                                                                                                                                                                                                                                                                                                                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was
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BB280255 KIKEN full-length enriched, adult retina Mus musculus cDNA
clone A930024N03 3' similar to AF217525 Homo sapiens clone cDSC1
comp syndrome cell adhesion molecule (DSCAM) mKNA, mKNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kiyosawa.H., Kojima, Y., Kondo, S., Koya.S., Kurihara, C., Kusakabe, M. Matsuyama.T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama.T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, C., Sato, K., Shibata, K., Shibata, C., Sato, K., Shibata, Y., Shiyemoto, Y., Shinagawa, A., Shiraki, T., Sodaba, Y., Y., Shiyemoto, Y., Taqawa, A., Takalashi, F., Tominada, N., Toya, Suzuki, H., Taqawa, A., Takalashi, F., Tominada, N., Toya, Suzuki, H., Suzuki, A., Watanabe, S., Yanamura, T., Yamanaka, I., Tuno, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, Yuno, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, Yuno, R., Yasunishi, A., Yoshida, K., Yoshiki, A., Yoshino, Yuno, R., Yasunishi, A., Yoshida, K., Yoshiki, A., Yoshino, Yuno, R., Yasunishi, A., Yoshida, K., Yoshida, K., Yoshiki, A., Yoshino, Yuno, R., Yasunishi, A., Yoshida, K., Yoshida, Y., Yuno, R., Yasunishi, A., Yoshida, K., Yoshida, Y., Yoshida, Y., Yoshida, Y., Yoshida, Y., Yoshida, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japrel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Usanici, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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    Y. and Hayashizaki, Y.
    Automated filtration-based high-throughput plasmid preparation

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pred. No. 1.9e-43;
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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BB333910 286 bp mRNA EST 11-JUL-2000
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BB333910 RIKEN full-length enriched, 10 days neonate medulla
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(DSCAM) mRNA, mRNA sequence.
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nilarity 55. 5;
Conservative
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/tissue_type="retina"
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/lab_host-"DH10B"
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RIKEN Shihide Hayashizaki

Contact: Yoshihide Hayashizaki

Taboratory for Genome Exploration Research (RIKEN)

The Institute of Physical and Chemical Research (RIKEN)

The Institute of Physical and Chemical Research (RIKEN)

The Institute of Physical and Chemical Research (RIKEN)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-44 (1999)
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                                                                                                                                                                                                           prepared and sequenced in Mouse Genome Encyclopedia prepared and sequenced in Mouse Genome Encyclopedia prepared and sequence in Riken Project of Genome Exploration Research Group in Riken PIKEN. Division of Experimental Animal Research in Riken PIKEN. Division of Experimental Animal Research in Riken PIKEN. Division of Experi
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/db_xret="taxon:10090"
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/dev_stage="10 days neonate"
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Oliqo-dT track not found. Not I site shown in beginning
is likely internal to the message.
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University of Nebraska, Lincoln
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Contact: Pomp, D
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                        of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5.6
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Pred. No. 5.6e-43;
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                                                                                                                                RS Konno, H., Akahira, S., Akiyama, J., Arakawa, T., Carninci RS Konno, H., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojimay, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Kiyosawa, H., Kojimay, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Noo, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, Y., Y., Shiqemoto, Y., Shinagawa, A., Shiraki, T., Soqabe, Y., Sugahara, Y., Y., Shiqemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, A., Watanabe, S., Yamamura, T., Yamanaka, I., T., Tsunoda, Y., Watahiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y., Muramatsu, M., and Hayashizaki, Y., Muramatsu, M., and Hayashizaki, Y., Shibata, Y., Vashihida, Watahabe, Y., Yashihida, Watahabe, Y., Yashihida, Watahabe, Y., Yashihida, Y., Yoshida, Y., Yoshiki, A., Yoshino, M., Wuramatsu, M., and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 20.7%;
Similarity 83.3%;
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB331669 280 bp mRNA EST 11-JUL-2000 BB331669 RIKEN full-length enriched, 6 days neonate medulla oblongata Mus musculus cDNA clone B730037M12 3' similar to AF217525 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule (DSCAM) mRNA, mRNA sequence.

BB331669 BB331669
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 280)
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                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                   Contact: Yoshihide Hayashizaki
1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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 Mismatches

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pred. No. 4.8e-42;
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Sciurognathi; Muridae; Murinae; Mus
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                                       Kanagawa 230-0045, Japan
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Best Local Similarity
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                                                                                                                                                      626
686 ctcct1gqtgqatac 700
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                                                                                                                                                                                                                                               tgtgagttqaattattccacqqicctcccccqtatqaattgatagcatggcaggagaagaa
                                                                                                                                                                                                                                                                                                                                           ATGCTACGAGCTTTGAAATCT-TTGATCTCAATCTCGGGAGGATCTGGGGGTTCTTGCAC
                                                                                                                                                                                                                                                                                                                                                                      atggtgcyayctltgacalctcltgatctcaatctcggggggatctggggggttcttgcac 565
                                                                                                                    accggaatetteteteactgttggcaaaatetgcagcgtagatatcaetteeteteceac 685
                                                                                                                                                                                                             224;
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URL:http://genome.gsc.riken.go.jp/
                                                                                            further details
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/dev_stage-"6 days neonate"
/lab_bust-"DH108"
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/clone="H730037M12"
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Pred. No. 9.9e-42;
Pred. No. 9.9e-42;
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Unpublished (2000)

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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
R., Okazaki,Y., Muramattsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramattsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Ttoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Okazaki
y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparatiou
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB334670 252 bp mRNA EST 11-JUL-2000 BB334670 RIKEN full-length enriched, 10 days neonate medulla BB334670 RIKEN full-length enriched, 10 days neonate medulla oblongata Mus musculus cDNA clone B830025103 3′s imilar to AF217525 Homo sapiens clone cDSC1 Down syndrome cell adhesion molecule
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                 contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer (5' GAGAGAGAGGATCCAAGAGCTCTTT: TTTTTTTTTTTVN 3'], cDNA was
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pred. No. 2.7e-273;
Mismatches 0;
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This cDNA clone codes for Down syndrome-cell adhesion molecule CC DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging CC to a novel subclass of the 1g superfamily with highest homology to CC to a novel subclass of the 1g superfamily with highest homology to CC technique was applied to bacterial and Pl artificial chromosomes CC technique was applied to bacterial and Pl artificial chromosomes CC between ETS2 and MX1 by using cDNA from trisomy 21 human foetal CC brain. A unique cDNA fragment, designated ES1 (see AAV31982), was CC brain and used to screen a trisomy 21 human foetal brain (14-wk CC obtained and used to screen a trisomy 21 human foetal brain (14-wk CC gestation) cDNA library. Further clones were obtained by exon CC trapping, and the complete DS-CAM2 cDNA sequence was identified. CC DS-CAM2 is a splice variant of membrane-bound DS-CAM1 (see AAW42086) and is deleted for the entire transmembrane domain. The DS-CAM cand is deleted for the entire transmembrane domain.
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signal transduction; trisomy 21; mental retardation;
holoprosencephaly; corpus (allosum agenesis;
schizencephaly; diagnosis; assay; human; ds; ss.
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CC 21q22.2-22.3. The invention also provides murine US-CAM partial CC sequences (see AAV31985-87), expression vectors and host cells, cransgenic animals, antisense oligonucleotides, and primers useful CC transgenic animals, antisense oligonucleotides, and primers useful CC associated with developmental and neurological processes. They can CC methods of repairing (regenerating) damaged or severed peripheral CC methods of repairing (regenerating) damaged or severed peripheral CC nerves. The products can also be used in detection, diagnostis and CC therapy of developmental and neurological abnormalities such as CC therapy of developmental and neurological abnormalities such as CC the corpus callosum, or schizencephaly. Antisense oligonucleotides care used for inhibiting translation of mRNA.
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                         ATCTCAGGGTTAATGATTCGGTCCTCCTTCTCCCAGCGGACTATAATGGGCTTCTCACCA
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No. 7.4e-148;
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                                               ATCTGCAGAGTAGAAATCACCTCTTCTCCCCACCTCCTTGGTGGACACAAGATAACGGGCC
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                                            the encoded polypeptides (AAM384A2-AAM42233) with nootropic, the encoded polypeptides of the inventor and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as localised neuropathies, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and shy-Drager Syndrome. Other uses include the activity of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic activity cancer diagnosis and therapy, drug screening, and assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
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Best Local Similarity
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The present sequence encodes one of 32 movel human secreted polypeptides. CC The nucleic acid molecules and polypeptides they encode may be used in CC the prevention, diagnosis and treatment of diseases such as CC immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus CC and human immuno-deficiency virus (HIV) infections), hyperproliferative CC and human immuno-deficiency virus (HIV) infections), hyperproliferative CC (e.g. Scimitar syndrome, chaga's cardiomyopathy and coronary CC (e.g. Scimitar syndrome, chaga's cardiomyopathy and coronary CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), CC (e.g. Huntington's chorea, CC (e.g. Huntingt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 4; 890pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ni J, Baker KP, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SOL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5720 BP; 1293 A; 1677 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their expression and activity.
                                                                                                AAT60757
                                                                                                                                                  AAT60757 slandard;
                                                 16-0CT-1997
                                                                                                                                                                                                                                                                                                611 atgycannanagaaaccynaatcttctctctcactyttggcaaaatctgcagcgta 665
                                                                                                                                                                                                                                                                                                                                                                                                 551 tgqggqtictiqcacidiqaqttqaaliaftccgcqgtcctccccgtatgaattgatagc 610
                                                                                                                                                                                                                                                                                                                                                                       TGGCTTTTCCTGCTAATCTGACGGCAATGGAGACAGAGTCGTATCCCAAGGCATTGGTGGC
                                                                                                                                                                                                                                                                        ATTGCAAGTGTAGAAACCCACATCTGCTTCCACTGGTGCCAAGATCTGTAAGGAA 3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wei P, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KP, Birse CE, Ebner
Moore PA, olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000Wo-0826014.
preferentially expressed gene 1.
                                                 (first
                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 22
Pred. No. 0.0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R, Fiscella M,
Rosen CA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1611 6; 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other:
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SA, Soppet
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Human aorti

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RESULT 7
AAZ510Z
ID AAZ510
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AC AAZ510
AC AAZ510
XX
OT 05-JUN
XX
DE Human
DE Human
XX
KW Aorta
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                                                                                                                                                                                                                                                                                                             Matches
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st Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; aortic preferentially expressed gene; APEG-1; aorta; specific; inhibition; growth; smooth; muscle; cell; vascular; proliferation; artery; restenosis; atherosclerosis; transplant; diabetes; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the human aortic preferentially expressed gene 1 (APEG-1) polypeptide, which is aorta specific and inhibits the growth of smooth muscle cells. The APEG-1 polypeptide can be used to inhibit vascular smooth muscle cell proliferation in an animal via its introduction into an artery of the animal. In an animal via the APEG-1 and the APEG-1 polypeptide can be products derived from APEG-1 and the APEG-1 polypeptide can be used to diagnose and treat vascular conditions, e.g. restenosis, atherosclerosis, transplant arteriosclerosis or diabetes. atherosclerosis, identified by differential expression in the aorta APEG-1 DNA, identified by differential expression in the aorta compared to ther organs, was used to obtain human APEG-1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09700953-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aortic preferentially-expressed gene APEG-1 - useful to develop prods, for diagnosis and treatment of vascular conditions, e.g. restenosis, atherosclerosis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Pages 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hsieh C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1225 BP; 249 A; 363 C; 382 G; 231 T; 0 other;
                                       Human aortic-preferentially-expressed gene-1 cDNA
                                                                     05-JUN-2000
                                                                                                AAZ51043;
                                                                                                                           AAZ51043 standard; cDNA;
                                                                                                                                                                                                                             652
                                                                                                                                                                                                                                                                     592 ccccqtatgaattgatagcatggcaggaqaagaaaccggaatcttctctctcactgttggca 651
                Human;
                                                                                                                                                                                                  318
                                                                                                                                                                                                                                                         378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-087380/08
                                                                                                                                                                                                                                                       CACCATACTCATTGACCGCTTTGCAAGTGTAGAAACCAGCATCGCCACGCTCTGCAGCCA 319
                                                                                                                                                                                                                 aaatctgcagcgfagatatcacttcctctcccacctcc
                                                                                                                                                                                                 GATCCGCAC CGCACAGCCCACCCTCAGCCTCCTCC
                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW10566
aortic-preferentially-expressed gene-1; APEG-1;
striated muscle cell; vascular smooth muscle ce
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee M;
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
78..419
/*tag= a
/label= APEG-1
                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US10636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9508-0494577
                                                                                                                                                                                                                                                                                                                            4.38;
                                                                        entry)
                                                                                                                                 1228
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                               Score 38.8; DB Pred. No. 0.056;
                                                                                                                                 θР
                                                                                                                                                                                                                                                                                                                  Mismatches
         smooth muscle cell; VSMC;
                                                                                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                   689
                                                                                                                                                                                                          .81
                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                               Length 1225;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                        Gaps
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The present sequence is a cDNA encoding aortic-preferentially-expressed components (APEC-1) protein from a human lambda gtl1 mortic 5'-stretch cDNA components (APEC-1) protein from a human chromosome 2933-34, components (APEC-1) protein isoforms, one specific to moscle cells designated APEC-1 protein and the other specific to components (APEC-1) protein can be administered to vascular smooth muscle cells (VSMC) to inhibit their proliferation or migration at the site of components (APEC-1) and the present sequence is used to screen VSMC-specific components (APEC-1) gene is useful to direct VSMC-specific expression. A components that bind to the repressor and components (APEC-1) gene is useful to discase such as alherosclerosis and restenosis.
                                                                                      RESULT 8
AAV48217/c
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    В
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                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarteriosclerotic; vasotropic; cis-acting transcriptional repressor; treatment; diagnosis; vascular disease; atherosclerosis; restenosis; chromosome 2q33-34; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New gene useful for treating and diagnosing vascular diseases comprises a single gene encoding aortic-specific and striated-specific muscle cell isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200009689-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 16; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY70077
                                                                                                                                                                                                                                                                                                      Sequence 1228 BP;
Human aortic preferentially expressed
                            09-NOV-1998
                                                    AAV48217;
                                                                            AAV48217 standard; DNA; 1238
                                                                                                                                                                                                     318 GGATCCGCAGCCGGGACAGCCCACCCTCCAGCCTCCTCC
                                                                                                                                                      652 aaatriqeagegtagataleaetteeteeteecaeetee
                                                                                                                                                                                        378 CACCATACTCATTTGACCGCTTTTGCAAGTGTAGAAACCAGCATCGCCACGCTCTGCAGCCA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-224334/19.
                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0134250
99US-0303069
                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US10298.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag- a
/product- "APEG-1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*Lag=
                                                                                                                                                                                                                                                                                                         249 A; 363 C;
                                                                                                                                                                                                                                                       4.3%;
                                                                                                                                                                                                                                           Score 38.8; DB 2
Pred. No. 0.056;
0; Mismatches 3
                                                                                                                                                                                                                                               0
                                                                                ВΡ
                                                                                                                                                                                                                                                                                                            382 G;
      gene-1
                                                                                                                                                                                                                                                                                                             231 T;
                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                        689
                                                                                                                                               281
                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                              3 other;
                                                                                                                                                                                                                                                                         Length 1228;
                                                                                                                                                                                                                                                  Indels
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RESULT 9
AAV48218/c
ID AAV482
XX AAV482
AC AAV482
XY 09-NOV
DT 09-NOV
XX Umman
XX ds; h
KW smooth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; human; aortic preferentially expressed protein 1; smooth muscle; cell proliferation; developmental stage; tissue plasminogen activator; p21 cell cycle; nitric oxide synthetase; gamma-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The aortic preferentially expressed protein 1 (APEG-1) can be used to derive an enhancer/promoter. This linked to a polypeptide coding sequence which regulates smooth muscle cell-specific expression of the polypeptide coding sequence can be used as a method of inhibiting vascular smooth coding sequence can be used as a method of inhibiting vascular smooth enuscle cell proliferation. The nucleic acids are used to direct developmental stage-specific expression of a heterologous polypeptide developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 16; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human, rat or mouse aorta or striated-muscle preferentially expressed proteins - useful for treating e.g. atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1238
ds; human; striated muscle preferentially expressed protein; smooth muscle; cell proliferation; developmental stage; gamma-interferon; tissue plasminogen activator; p2l cell cycle; nitric oxide synthetase.
                                                                                  Human striated muscle preferentially expressed gene
                                                                                                                                                                                                                     AAV48218 standard; DNA;
                                                                                                                                   09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                               328 GGATCCGCAGCCGGCACAGCCCACCCTCAGCCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
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                                                                                                                                                                                                                                                                                                                                                                   aaatetgeagegtagatateaetteeteteeaeetee 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9705-0795868
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
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88..429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "No start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 A; 365 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Aortic-preferentially-expressed start codon given"
                                                                                                                                                                                                                               2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.8; DB pred. No. 0.056; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DH 19;
                                                                                                                                                                                                                                                                                                                                             291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 10
AAZ51044/c
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                                                                                                                                                                                                                                                      В
Query Match

Best Local Similarity 62.

Matches 61: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The striated muscle preferentially expressed protein (SPEG) can be linked to an enhancer/promotor derived from an aortic preferentially expressed gene to regulate smooth muscle cell-specific expression. This can be used as a method of inhibiting vascular smooth muscle cell proliferation. The nucleic acids are used to direct developmental stage-specific expression of a heterologous polypeptide which is stage-specific expression of a heterologous polypeptide which is especially selected from tissue plasminogen activator (tPA), p21 cell expression, nitric oxide synthetase, gamma-interferon, atrial cycle inhibitor, nitric oxide synthetase, gamma-interferon, atrial cycle inhibitor, nitric oxide synthetase, gamma-interferon strial cycle inhibitor. These are used to inhibit the proliferation of smooth muscle cells, e.g. for the treatment of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9835040-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human, rat or mouse worth or striated-muscle preferentially expressed proteins - useful for treating e.g. atherosclerosis \mbox{\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-447237/38
P-PSDB; AAW77048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Fig 20; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hsieh C,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2793 BP; 499
                                                                                                                                                                                                                                                                                                           1947
                                                                                                                                                                                 AAZ51044 standard; cDNA;
                                                                                                                                                                                                                                                      1887
                        Human; striated muscle preferentially expressed gene; SPEG; aortic-preferentially-expressed gene-1; APEG-1; striated muscle cell; aorta; smooth muscle cell; antiarteriosclerotic; vasotropic; treatment; diagnosis; vascular disease; atherosclerosis; restenosis;
                                                                                                                                                       AAZ51044;
                                                                                                                                                                                                                                                                                                                        592 recentargualinatuncutyneungagadanenggaatetteteteaetgttggca 651
                                                                                              Human striated
                                                                                                                             05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                    GGATICCGCAGCCGGCACAGCCCACCCTCAGCCTCCTCC
                                                                                                                                                                                                                                                                       aaatrigeagegtagalateartteeteteecacetee
                                                                                                                                                                                                                                                                                                          CACCATACHCAPPGACCGCPPPGGAAGTGTAGAAAGCAGCATCGCCACGCTCTGCAGCCA 1888
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0795868
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                muscle preferentially expressed gene partial cDNA.
                                                                                                                                                                                                                                                                                                                                                                                     6.2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ct- "Striated muscle preferentially expressed protein"
"No start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 963
                                                                                                                                                                                       2793
                                                                                                                                                                                                                                                                                                                                                                         <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                      Prod. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç
                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                 920
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      .8.85
                                                                                                                                                                                                                                                                                                                                                                                                                                               ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                          8; DB 19;
0.085;
                                                                                                                                                                                                                                                               1850
                                                                                                                                                                                                                                                                                           689
                                                                                                                                                                                                                                                                                                                                                                               : 78
                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                            2793;
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RESHLT 11
AAQ25532/c
ID AAQ255
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AAQ255
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AC AAQ255
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Z2-NO)
DT 22-NO)
DT 22-NO)
DY Sequer
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ches 6
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a partial cDNA encoding human striated muscle preferentially expressed gene (SPEG) protein. This protein was detected in striated muscles of skeletal and cardiac tissues. Was detected in striated muscle cell protein isoforms encoded by It is one of the two muscle cell protein isoforms encoded by the aortic-preferentially-expressed gene-1 (APEG-1) located on human chromosome 2q33-34. The other protein isoform is specific to aortic smooth muscle cells designated APEG-1 protein. The present sequence can smooth muscle cells designated APEG-1 specific-promoter which may be be used to identify striated muscle cell specific-promoter which may be used to direct gene expression in striated muscle cells to treat diseases associated with these muscles. APEG-1 gene is useful for treating and diagnosing vascular diseases such as atherosciarosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200009689-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New gene useful for treating and diagnosing vascular diseases comprises a single gene encoding aortic-specific and striated-specific muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 29; Fig 20; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell isoforms
                                                                                                                                                                                                                      1887
                                                                                                                                                                                                                                                                         1947 CACCATACTCATTGACCGCTTTGCAAGTGTAGAAACCAGCATCGCCACGCTCTGCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2793 BP;
                                                                                                                                                  AAQ25532 standard; DNA; 1648
                                                                                                                                                                                                                                                                                                     592
                                                   Sequence of genomic clone protein (HisRP) gene.
                                                                                                                        AAQ25532;
  plasmodium lophurae
                          Målaria vaccine; Histidine-rich protein; cytoadherence;
                                                                                                22-NOV-1992
                                                                                                                                                                                                                                             652 adatotycagoytagatatoacttoctotoccaccino 689
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                                                                                                                                                                                                                                                                                        coccytatgaartgalaycalgycaygagaagaaaccydaalcttetetcactyltogca 651
                                                                                                                                                                                                                      GGATTCCGCAGCCGGCACACCCTCAGCCTCCTCC 1850
                                                                                                                                                                                                                                                                                                                            4.38;
1 Similarity 62.28;
61; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hsieh C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70078.
                                                                                               (first entry)
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99US-0303069
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/product=
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                      499 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SPEG protein"
                                                                                                                                                                                                                                                                                                                                                                                                      963 C; 920 G; 411 T; 0 other;
                                                                       conty.
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                        ВP
                                                                          the entire Histidine-rich
                                                                                                                                                                                                                                                                                                                                                                38.8;
                                                                                                                                                                                                                                                                                                                                                     0.085;
                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                   Length 2793;
                                                                                                                                                                                                                                                                                                                                          indels:
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                        1888
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Two variants of HiskP are produced by P. falciparum. One is associated with what is referred to as "knobby phenotype" (K3) and associated with what is referred to as "knobby phenotype" (K3) and associated with what is referred to as "knobby and "knobless" phenotypes ("knobbes phenotype" (K-). The "knobby and "knobless" phenotypes of the pressing in cytoadherence, which is characteristic of the both K+ and K- HiskP can be obtained by the use of P. lophurae HiskP concerns the grounding the sended in two expressing that the sended to the sequence from the genome. The sequence of the protein occurs via the proposition, obtain probes spiritle bomologous DNA sequences in a confidence of the protein sequence. The sequence of mature proteins is arranged to the proposition and the sequence of mature proteins is arranged from unmerous tandem repeats with up to nine histidine residues in a confidence of the protein of the protein of the protein collect Plasmodium proteins for which sequence data
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 Вþ
                                                                                                                 Query Match
Best Local
                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5116965-A
                                                                                                                                                                                                                                                                                                                                                                                                                                     Histidine-rich protein associated with Plasmodium knob phenotype and DNA encoding it, used for in vitro diagnosis of P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pologe L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 7A-B; 20,000 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-199590/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SLOK ) SLOAN KETTERING
                                                                                                                                                                                                                                                                                                                                                                                                                          Falciparum
                                                    1390
                                                                                                                                                                   Sequence 1648 BP;
  1330
                                                               267 Leegeegtgalgglgaleelegtlgelgggeteaclettgeeaateeggttettggegtae 326
                           327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _peptide
ATCCTGATCATGATGCTGCTGCTGGTGCATCGTGATGATGATGGTGGTGGT 1278
             atgcqqatqctqtagqtqqaqgaaggatqqatatcaatgatgqtgqccqaqtt 379
                                                66;
                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             infection.
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag- e
/label- splice :
563..1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8605-0900401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag- 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8608-0900401
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485..490
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360..490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*Lay-
                                                                                                                                                                                            reported.
                                                                                                                                                                        569 A;
                                                                                                                     4.2%;
58.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INST CANCER
                                                                                                                                                                        4H8 C;
                                                                                                         0;
                                                                                                                    Score 37.8; DB 13; pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                          150 G;
                                                                                                          Mismatches
                                                                                                                                                                           441 T; 0 other;
                                                                                                             47;
                                                                                                                                    Length 1648;
                                                                                                              Indels
                                                                                                                0;
                                                                                                                Gaps
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RESULT 12 AAH25568/c

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`\2555555555555555555555555555
                                                                                                                                                                                                                                                                                             Ax The present sequence encodes an interferon omega-1 like protein, cc designated NoV2. The protein is a membrane bonn, a secreted protein. Cc designated NoV2. The protein is a membrane bonn, a secreted protein. Cc preventing a NOV-associated disorder, and in the manufacture of a preventing a NOV-associated disorder, and in the manufacture of a cc as NOV-associated disorder. They are also useful for treating disorders as NOV-associated disorder. They are also useful for treating disorders cc as NOV-associated disorder. They are also useful for treating disorders cc and activation of thymic immune cells, pathologies related to germatogenesis and male infertility, diagnosis of several human cc spermatogenesis and male infertility, diagnosis of several human cc such as red blood cells and platelets, various immunological disorders cand/or pathologies, autoimmune and inflammatory diseases, cardiovascular diseases, metabolic diseases, cancer growth and cells the control of the control of the control of the cardiovascular diseases, metabolic diseases, neurodecenerative disorders, and the control of the co
Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blood circulation; immunological usokase; metabolic disease; inflammatory disease; cardiovascular disease; metabolic disease; inflammatory disease; cardiovascular disease; neukemia; glioma; cancer; viral intection; acute lymphoblastic leukemia; glioma; cancer; viral intection; acute lymphoblastic leukemia; glioma; enurological disease; neurological disease; neurological disease; hematopoietic disorder; neurodegenerative disorder; parkinson's disorder; hematopoietic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH25568 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; blood circulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of an interferon omega-1 like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH25568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferon omega·1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1999;
10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides designated as NOV polypeptides, useful in detection, prevention and treatment of a broad range of pathological states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB84469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prayaga SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 15-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                 leukemia, in gliomas, neurological diseases, neurodegenerative disorders. Alzheimer's disease, Parkinson's disorder, and hematopoietic disorders. NOV polypeptides and polynucleotides are also useful for treating neurodegenerative disorders, immune disorders and hematopoietic
                                                                                                                         Sequence 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0169887
99US-0170230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "interferon omega-1 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spermatogenesis; male infertility; neoplasia; immunological disorder; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      like protein:
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                                                                                                                                   259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92pp; English.
                                  4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA.
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                                                                                                                                   Α.
                                                                                                                                      736
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          Score 37.2; D. pred. No. 0.22 0; Mismatches
                                                                                                                                         Ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nov2; membrane bound protein;
                                                                                                                                         577
                                                                                                                                         ç;
                                                                                                                                           315 T;
                                           DВ
. 22;
                                                                   22;
                                                                                                                                           0
                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein NOV2"
                     Indels
                                                                Length 1887;
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                          0;
                          Gaps
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RESULT 13
AA164010/c
ID AA1640
XX AA1640
XX 22-OCT
XX Human
XX Human;
XW Cerebr
KW Cerebr
KW ceredio
KW antiin
KW antiin
KW antiin
XX WO2001
XX WO2001
XX Homo s
XX 1-JAN
PR 11-JAN
PR 11-JAN
PR 11-MAF
PR 11-MAF
PR 11-MAF
PR 11-JUL
PR 11-
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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11-JUL-2000)
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24-FEB-2000;
02-MAR-2000;
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2000US-0180628.
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2000US - 0220964

2000US - 0224518

2000US - 0224513

2000US - 0225214

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The invention relates to human polynucleotides (AA163803-AA164012) and CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The CC specification. The nucleic acids, proteins, antibodies and (ant)agonists (CC specification. The nucleic acids, proteins, antibodies and (ant)agonists (CC e.g. breast and ovarior cancer and other cancers of the adrenal gland, (CC e.g. breast and ovarior cancer and other cancers of the adrenal gland, (CC e.g. breast and ovarior cancers and other cancers of the adrenal gland, (CC croim's disease, multiple scalerosis, recumancial architis and ulcerative (CC croim's disease, multiple sclerosis, recumancial architis and ulcerative (CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and (CC epilepsy; and (f) infections diseases such as viral, bacterial, fungal (CC and parasitic infections diseases such as viral, bacterial, fungal) (CC and parasitic infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC and parasitic infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases such as viral, bacterial, fungal) (CC constant) infections diseases (
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                                                                                                                                                                                                                              Sequence 8269 BP; 1826
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gttyssffallocsocggtoctocccgtalgasttgatsgcatggcaggagaagasaccgg 630
                                                                              gogagotilqacaletetigaloteaaleteggggaggatetgggggttettgeaetgtga 570
                                                                                                                                 l Similarity
81; Conserv
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2000US-0251999.

2000US-0254978.
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                                                                                                                                     Conservative
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RESULT 14
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                                                                                                                                                                                                                                                                                 The present sequence represents a Pseudomonas aeruginosa nucleic aicd sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a p. aeruginosa infection.

is a p. aeruginosa infection.

is a p. aeruginosa infection.

is a p. aeruginosa sumptions were made as to the identity of the base; in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virulence factors useful in developing
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les 97; Conserv
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                                                                                                                GCTCUCCTGGGGGAATGACGGTGGTCTTTCTGAACGGGTTGACTTGGGAUTGCGTCACC
                                                                                                                             gttcagctgaggggaaacatctttggttctctgagcagaatcccacgagtctgatttatt 436
                                                       AACTCATGCTCGATGGCATAGCCCCAGATCGTCCGCAGATvATTCGAGTACGTGTTCCAG
                                                                        tttgcattcacactgtcatagcctgtgatgyggctgttgccatcaaaccccatggtccac 496
CTCCGCTTGGACAGGCCTTGTTCCAGTACCTTGCGTCGCCATCCCAGGACAGCCCGGTGG
                  ctgagcgtgatggtgcgagctttgacatctcttgatctcaatctcgggaggatctgggyg
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milarity 49.28;
Conservative
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pathogenic infection; Pseudomonas aeruginosa infection;
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                                                                                                                    21791 GUTUGGCTGGGGGAATGACGGTGGTCTTTCTGAACGGGTTGACTTGGGAGTGCGTCACC 21732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence factors useful in developing
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                                                                                                                                                                                                                                                                                                   is a p. aeruginosa injection. onote: the sequences given in the specification were poorly legible, and note: the sequences given in the sequence as to the identity of the base; in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely it is therefore possible that the sequence given below is not entirely.
                                                                                                                                                                                                                                                        Sequence 42235 BP;
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                                                                                                                                    gttcagcigaggggaaacatctttggttctctgagcagaatcccacgagtctgatttatt 436
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CTCCGCTTGGACAGGCCTTGTTCCAGTACCTTGCGTCGCCATCCCAGGACAGCCCGGTGG
                                                          AACTCATGCTCGATGGCATAGCCCCCAGATCGTCCGCAGATGATTCGAGTACGTGTTCCAG
                                                                           tttgcattcacactgtcatagcctgtgatggggctgttgccatcaaaccccatggtccac 496
                 ctgaqcglyatggtgcgagctttgacatctctttgatctcaatctcgggaggatctggggg 556
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an M. Tsongalis
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Pred. No. 1.
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Perfect score:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
nucleic search, using sw model
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Match Length
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  tgccggccggttgcaagcct.....gcgcccacatcgttcgctga 898
  1 US-08-494-577-11
2 US-08-795-868-13
3 US-08-795-868-13
3 US-08-232-463-14
4 US-08-494-577-2
4 US-08-494-577-1
5 US-08-494-577-1
5 US-08-68-395A-2
6 US-08-68-395A-2
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Query Match 4.3%; Score 38.8; DB 1; Le Best Local Similarity 62.2%; Pred. No. 0.0056; Matches 61; Conservative 0; Mismatches 37; 1	US-08-494-577-11/c US-08-494-577-11/c US-08-494-577-11/c Sequence 11, Application US/08494577 Sequence 11, Application US/08494577 Sequence 11, Application US/08494577 Patent No. 5786171 GENERAL INFORMATION: APPLICANT: Lee, Mu-En APPLICANT: Lisieh, Chunq-Minq APPLICANT: Lisieh, Chunq-Minq APPLICANT: Lisieh, Chunq-Minq APPLICANT: Lisieh, Chunq-Minq APPLICANT: US-05-12 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: US-A ZIP: 02110-2804 COMPUTER: LIMP PC compatible	C 28 29.8 3.3 1335 3 US-09-167-354-5 3
Length 1225; Indels 0;	GENE AND	Sequence 6, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 30, Sequence 30, Sequence 41, Sequence 41, Sequence 41, Sequence 41, Sequence 41, Sequence 41, Sequence 32, Sequence 32, Sequence 33, Sequence 33, Sequence 33, Sequence 34, Sequence 3, Sequence 3,

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                                             Patent No. 5846773
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Rest Local Similarity 62.2%;

Matches 61; Conservative
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/494,577

APPLICATION UNMBER: 08/494,577

FILING DATE: 22-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819
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INFORMATION FOR SEQ ID NO: 11:
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APPLICANT: Hsieh, Chung-Ming
APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
TITLE OF SEQUENCES: 19
                                    GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson, P.C.
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TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
APPLICANT: Lee, Mu-En
APPLICANT: Hsieh, Chung-Ming
                                                                                                                                                                             652 aaaletgeageglagataleaetteeteeteeeaeelee 689
                                                                                                                                                                                                                                                  592 coccqtatgaaligatagcalqgcaggagaagaaarcqqaalcttctctctcactgttiggca 651
                                                                                                                                                                                                                                 388 CACCATACTCATTGACCGCTTTGCAAGTGTAGAAACCAGAATCGCCACGCTCTGCAGCCA 329
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06-FEB-1997
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                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                           Score 38.8; DB 2; Length 1238; Pred. No. 0.0057;
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; LOCATION: 3...198
; OTHER INFORMATION:
US-08-795-868-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                          GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Kichardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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MEDIUM TYPE: Diskell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,819
REFERENCE/POCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA
                                                                                       APPLICANT: DÖRNER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FAIKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CON
OPERATING SYSTEM:
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Coding Sequence
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                                           CITY: Alexandria
ZIP: 22313-0299
            COUNTRY:
                               STATE:
                                                          STREET:
                                                                           ADDRESSEE:
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02110-2804
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                                                            1800 Diagonal Road, Snite 500
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                                                                           Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38.8; DB 2;
Pred. No. 0.0092;
U; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2793;
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US-08-232-463-14
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                                                                                                                                                                                                      Sequence 2, Application US/08494577 Patent No. 5786171
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MEDJUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMBUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                              GENERAL INFORMATION:
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NAME: BENT, Stephen A.
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LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                    APPLICANT: Lee, Mu-En
APPLICANT: Heich, Chung-Ming
APPLICANT: Heich, Chung-Ming
TITLE OF INVENTION: AORTIC PREFERENTIALLY EXPRESSED GENE AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 12
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CORRESPONDENCE ADDRESS
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MOLECULE TYPE: DNA
US-08-494-577-2
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Best Local Similarity 60.8%;
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 F
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                             APPLICANT: Lee, MI-2:
APPLICANT: HSteh, Chord-Ming
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592 ccccqtaidaaltgatag, iggcagqaqaagaaaccggaatcttctctctcactgttggca 651
                            SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,868
FILING DATE: 06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GGAPCCTCAACCGGGAAAGCCCAACCGTCGGCCTCCTC
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STRANDEDNESS: single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                         COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                             STREET:
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                 CLASSIFICATION:
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                                                                                                              IBM Compatible
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pred, No. 0.019;
0; Mismatches 38;
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                                            TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTEKISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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st Local Similarity 60.8%;
atches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/494,5
FILING DATE: 22-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
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APPLICANT: Hsich, Chung-Ming
TITLE OF INVENTION: AORTIC PREFERENTIALLY EXPRESSED GENE AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/06 FILING DATE: 22-JUN-1995 CLASSIFICATION: 436 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Florpy
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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MOLECULE TYPE:
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                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                               NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/012001
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US-08-494-577-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                         Query Match 4.0%;
Best Local Similarity 60.8%;
Matches 59; Conservative
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TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 1:
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TITLE OF INVENTION: A SINCLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVENTION: AND SCRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DAS
SOFTWARE: FASISED for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM MEDIUM TYPE: Diskett
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APPLICANT: Hsiel
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/494,577
FILING DATE: 22-JUN 1995
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NAME: Fraser, Jamis K
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                                                                                592 ccccgtalgaattgalaycalygcaggagaagaaaccggaatcttctctcactgttggca 651
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ZIP: 02110-2804
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CITY: Boston
410 GGATCCTCAACCGGCAGAGCCCACCCTCGGCCTCCTC 374
                              652 aaatotgoagoglagalatoacttoctotoccacoto 688
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                             I NEOKMAT TON
                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                05433/032001
                                                                                                                                0; Mismatches
                                                                                                                                            Score 36.2; DB Pred. No. 0.043;
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                                                                                                                                                              DB 2;
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                                                                                                                                                                Length 1308;
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JS-08-068-395A-2/c
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Patent No. 5496719
US-08-068-395A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 68-2.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
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FILING DATE: 1930527
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-135254
FILING DATE: 27-MAY-1992
PRIOR APPLICATION NUMBER: JP 5-44013
APPLICATION NUMBER: JP 5-44013
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-44014
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APPLICANT:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: HOSHINO,
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APPLICANT: ¿DEKOBA, CHIE
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LENGTH: 1755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
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                                                                                                                                             LOCATION:
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KAJINO, TSUTOMU
IMAEDA, TAKAO
SAKAI, KIYOKO
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110..1624
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                                  mat_peptide
170..1624
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110..169
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Best Local Similarity 56.1%;
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APPLICANT: YAMADA
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FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-4
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
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                                                                                                                           TELEFAX: (703) 413-2221
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC comparible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 GURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 5-440
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5700659man
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1755 S. CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                         TELEPHONE: (703)
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
Y: U.S.A.
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                                                      nucleic acid
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                              1755 base pairs
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IMAEDA, TAKAO
SARAI, KIYOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDEKOBA, CHIE
HOSHINO, FUMIHIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUGIYAMA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 5-44013
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0; Mismatches 47; Indels
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Pred. No. 1.
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                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1)..(1554)
US-09-043-123-1
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Best Local Similarity 56.1%;
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1995-09-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HAAS, Rainer
APPLICANT: ODENBREIT, Stefan
APPLICANT: MEYER, Thomas F.
APPLICANT: BLUM, Andre
APPLICANT: BLUM, Andre
TITLE OF INVENTION: NEW ADHESIN FROM HELICOBACTER PYLORI
FILE REFERENCE: 05648004
                                                                                                                                                                     Query Match
Best Local Simila ity
Matches 77; conserv
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/043,123A CURRENT FILING DATE: 1998-06-26 EARLIER APPLICATION NUMBER: DE/195 35 321.8
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                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                               LENGTH: 1557
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    .1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                       1186 aatttyctcacttatggygtggggactgatgtgctttaraatgtgtttagccgctctttt 1245
                                                                                                                               668 tatcacttcctctcccacctccttggtggatacagtacgggccactttcaggggtLaatga 727
                                                                     728 teciqtetetetetecageggacaatgatgggeteteccatgggetgtgcageteatte 787
ggtagtaggaglcttaatgcgggcttctttggg 1278
                  cttcctttgaccctgatggccaggtggtgtggg 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09043123A
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170..1624
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110..1624
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110..169
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                                                                                                                                                                                           Score 31.4; DB 3; Length 1557; pred. No. 1.9;
                                                                                                                                                                                 Mismatches 76;
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; TYPE: nucleic
; STRANDEDNESS:
; TOPOLOGY: line
US-08-324-243-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATE: 19-SEP-1277
FILING DATE: 19-SEP-1277
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786
REFERENCE/DOCKET NUMBER: 00786
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 542-5070
TELEPAN: (617) 542-8906
TELEX: 2 0154
INFORMATION F-R-SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
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Patent No. 5786464
GENERAL INFORMATION:
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US-08-532-390-34/c
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                                                                                                                                                                                                                                                                                  Sequence 34, Application US/08532390 Patent No. 5795737
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-120S/MS-120S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                    APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: High Level Expression of Proteins
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225 Franking
CITY: Boston
STATE: Massachusetts
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                 495 GTTGGTGGTGCTCAGGTCAGGTCAGTTCAGGGTCACGCACAGGGGGGTCAGCTTCA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/324,243 FILING DATE: 19-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                         323 gtacalurygalurclylagulygagulagagulygatatcaatgatggtggccgagttca 381
                                                   STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                            STATE: Massa
                                                                                                                                 STREET:
                                                                                                                                                   ADDRESSEE:
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                                                                                                                                     225 Franklin Street
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US-08-717-294-34/c
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Matches 64: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6114148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/POCKET NUMBER: 00786/294001
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
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                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
                                                                                                                                                                                                                                                     ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF TITLE OF INVENTION: PROTEINS
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                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LECH, KAREN F.
REGISTRATION NUMBER: 35,238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                    SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
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TELEX: 200154
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                                                                     FILING DATE
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PCT-US95-11511-34/c
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Best Local
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
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ZIP: 02110-2804

COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: 15M PC compatible
COMPUTER: 15M PC compatible
SOPTWARE: Fatenth Pelcase #1.0, Varsion #1.30B
SOPTWARE: Fatenth Palacase #1.0, Varsion #1.30B
COMPRENT APPLICATION NUMBER: Pal/US95/11511
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ADDRESSEE: Fish & Richardson
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,
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COUNTRY:
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STATE: Massa
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AL214561 "Etraodon
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AL027133 Fugu rubr
AL027123 Fugu rubr
AL014935 F.rubripe
AL027127 Fugu rubr
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REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE ORGANISM RESULT BF348620 LOCUS COMMENT ACCESS ION DEFINITION FEATURES JOURNAL source cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 05 Plate: LLAM9426 row: p column: 05 High quality sequence stop: 697. 1 (bases 1 to 744) NIH-MCC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D. ##348620 744 bp mRNA EST 22-NOY-2000 602019924F1 NC1_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155508 5', mRNA sequence. Eukaryota; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens EST. human. BF348620.1 G1:11296215 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4155508" /clone_lib="NCI_CGAP_Brn67" Location/Qualifiers 22-NOV-2000

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                           Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
                                                                                        Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.S., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-mcKown, C.G., Pericea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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188457 MARC
                                                                             Keele, J.W.
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 196 c 210 g 150 t
                                                                                                                                                                                      Metazoa; Chordata; Craniala; Vertebrala; Euteleostomi;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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87.3%;
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                                                                                                                                          HF528580 712 hp mRNA
602043580F1 NC1_CGAP_Brn67 HC
5', mRNA sequence.
BF528580
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PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                              Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAG:TATGACGAT
BACKWARD: GTTTTCCCAGTACGACG
Plate: 98 row: A column: 1
Seq primer: ATTTAGGTGACACTATAG.
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Contact: Robert Strausberg,
            Unpublished (1999)
                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                      Homo sapiens
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a 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"MARC 4BOV"
/tissue_type-"pooled"
/lab_host-"DH10B"
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/db_xref="taxon:9913"
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Pred. No. 1.4e-62;
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                                                                                                                   AACAATAGAAGCTTTGACAC
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Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLAM9493 row: p column:
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CNS02UJS 1008 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
167120 of library G from Tetraodon nigroviridis, genomic survey
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/note="Organ: brain; Vector: pCMV-SPORM'6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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/clone_lib-"NCI_CGAP_Brn67"
/Lissue_type="anaplastic oligodendroglioma with
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60.0%;
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Pred. No. 1.6e-28;
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                                                                                  Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases | to 1008)
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AL214561.1 G1:7873380
GSS; genome survey sequence.
Tetraodon nigroviridis.
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Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases this sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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2 (bases 1
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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а 267 с
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/db_xret."Laxom:99883"
/elone-".7720"
/clone-".7720"
/clone-".760moscope sequence ID : COAG167BE1OSP1-end
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DEFINITION LOCUS

HSC2XA021 normalized

F13426

310 bp

INRNA

infant brain cDNA Homo sapiens cDNA clone

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IMAGE: molecular integration of the analysis of the human genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: (-21)M13_universal.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                     Homo sapiens
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/dev_stage="3 months old"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="forgan: brain; Vector: lafmid BA; Site_1: HindIII;
/note="forgan: brain; Vector: lafmid BA; Site_1: HindIII;
/stolate=muscular atrophy patient; tissue_type=total brain
/stolate=muscular atrophy patient; tissue_type=total brain
/stolate=muscular atrophy patient; tissue_type=total brain
/stolate=muscular atrophy patient;
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/db_xref="taxon:9606"
/clone="c-2xa02"
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Pred. No. 9.3e-13;
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                      Craniata; Vertebrata; Enteleostomi;
Catarrhini; Hominidae; Homo.
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Auffray,C., Hehar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
,M.D., Duprat,S., Honlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
Sebastiani-Kabaktchis,C. and Tessier,A.
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C. R. Acad. Sci. I
95277534
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Seq primer: (-21)M13_universal.
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 Takifugu rubripes.
Takifugu rubripes
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                                                                                                        Eukaryota; Metazoa; Chordala; Craniala; Vertebrala; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoreleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontilormes;
                                                                                                                                                                                           AL014925.1 G1:2681293
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Centre Hinxton, Cambridge,
Vector: pBluescript II KS
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/dev_stage="3 months old"
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/sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"taxon:9606"
/clone-"c-zwh04"
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89.7%;
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Pred. No. 4.9e-12
0; Mismatches 1
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Cedex, FRANCE
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          Query Match 9.3%;
Best Local Similarity 69.7%;
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PRIMER:
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                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource
Submitted (19-JUN-1998) MRC Human Genome Mapping Project Resource
Control Hinxton, Cambridge, CB10 1SB, UK. Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ.027133.1 GI:3264476
GSS: genome survey sequence.
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Takifugu rubripes
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Elgar,G., Clark,M., Smith,S., Meek,S.,
                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                    biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
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/db_xref="taxon:31033"
/clone_lib="cosmid 070M05"
/clone="070M05aA12"
/ 152 c 124 g 137 L
                                                                                             /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone=lib="cosmid 096F20"
/clone="096F200"
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153 c 154 g 168 t
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                 Score 46.4; DB 13; Pred. No. 0.018;
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Best Local Similarity 53.5%;
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1 (bases | to 601)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Breuner,S.
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Takitugu rubripes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pHluescript II KS
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GSS; genome survey sequence.
Takifiygu rubripes.
Takifiygu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Euteleostei; Neoteleostei;
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/db_xref-"taxon:31033"
/clone_lib-"cosmid 070M05"
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Matches 58
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                                                                                                                                                                          Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda,
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-JUN-1998) MRC Human Genome Mapping
Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMEN: KS
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1 (bases 1 to 614)

1 (bases, Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
                                   http://www.niddk.nih.gov/intram/people/boliver.htm Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (See http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
                                                                                                                                                                                                                                                                                                              Genome Res. 10 (12), 2030-2043 (2000) 20568492
                                                                                                                                                                                                                                                                                                                                                        Gene discovery using computational and microarray analysis transcription in the drosophila melanogaster testis
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1 (bases 1 to 412)
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                                                                                                                                                                                                                                                                                          On Aug 17, 1999 this sequence version replaced gi:5735990
                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and
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Seq primer: M13RP1 reverse primer (ABI).
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/clone="096F20cC11"
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/db_xref="taxon:31033"
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RESULT 12
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Best Local Similarity
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                                                                              http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 47 row: f column: 09
                                                                                                                                                                                                                                         Laboratory of Cellular and Developmental Biology MIDDK, National Institutes of Health 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethe Fax: (301) 496 5239 Email: Oliverthelix.nih.qov.
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                   Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .617
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Contact: Brian Oliver
                                                                                                                                                                                                                                                                                                                                                                                                         Andrews, J., Bouffard, G. and Oliver, B. Drosophila melanogaster testis expressed
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1 (bases 1 to 617)
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/strain="y[*] w[67c1]/Y"
/db_xref-"taxon:7227"
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/lab_host="SOLR (Stratagene)"
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/organism="Drosophila melanogaster"
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Pred. No. 1.1;
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RESULT 13
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AUTHORS
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                                                                                                                                                                                                                                                                                                                            Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, km Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@hellx.nih.gov
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                                                                                                                                                                                                 http://www.niddk.nih.gov/intram/people/boliver.htm Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (see http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural
                                                                                                                                                        Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 61 row: d column: 09
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Drosophila melanogaster testis expressed sequence tags
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                                                                                                     primer: M13RP1 reverse primer (ABI).
    Location/Qualifiers
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/note="Organ: testis; Vector: pBlueScript SK (Stratagene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
/organism-"Drosophila melanogaster"
/strain="y[*] w[67c1]/Y"
/db_xref-"taxon:7227"
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/db_xref="taxon:7227"
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Pred. No. 1.
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Local Similarity 62.6%;
hes 62; Conservative
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Celniker, S. and Rubin, G.M.

HIGP/HHMI AT Drosophila EST Project
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Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11569613.
Contact: Stapleton, M.
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BF486312.2
                                                                                                                                                                                                                                                             High quality sequence stop: 519.
                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, esi@fruitfly.berkeley.edu
hit genomic AE003460: arm:2R []8105561,18403467]
estimated-cyto:59D2-59E1: 04/09/2001
Plate: AT.205 row: G column: 4
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Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
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/clone="AT20576"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                                                                                /organism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
                                                                                                                                                                                                                 Location/Qualifiers
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/lab_host-"SOLR (Stratagene)"
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Matches 62; Conserv
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Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 54 row: f column: 11
Seq primer: MISRPI reverse primer (AHI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, km Bl-13, Helhesda, MD 20892 USA
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Brian Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota;
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Drosophila melanogaster testis expressed sequence tags
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/dev_stage="0-3 day old ore-R males"
/dev_stage="0-3 day old ore-R males"
/lab_host="Plates AT.10-AT.120; DH5-alpha. Plates
AT.121-AT.319; DH5-alpha TonA"
AT.121-AT.319; DH5-alpha TonA"
/note="0rgan: ADULT testes; Vector: pOTB7; Site_1: Ecoki;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
day old Ore-R males. RNA kindly provided by the lab of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library." 202 c 167 g 105 t
                       /note-"Organ: testis; Vector: pBlueScript SK (Stratagene); Site_1: EcoR I; Site_2: Xho '; Testes lissected from 1-5 day adult y[*] w[67c1]/Y males raised at 250C. RNA isolated using Trizol (Life Technologies) and a single
                                                                                                                                                                                                                          /organism="prosophila melanogaster"
/strain="y|*| w[67c1|/Y"
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/cione="bs54f11"
round of Poly(A)+ selection using Oligotex
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/lab_host="SOLK (Stratagene)"
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library constructed using Stratagene ZAP-cDNA syntesis kit. Oligo dr-primed, size fractionated ~1-6 kb, and directionally cloned at EcoRI and XhOI in Uni-ZAP XR. Following a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be homored.
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δÃ Query Match 7.9%; Best Local Similarity 62.6%; Matches 345 teginaceateteetgeateetgqteggggttetaetgetetttgtgettetgetggttg 404 62; Conservative u; Mismatches Score 39.8; Di Pred. No. 1.3; DB 11; 37; ludels Length 646; 0; Gaps

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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New isolated bown's Syndrome-cell adhesion molecule -develop products for detection, diagnosis and therapy developmental and neurological abnormalities

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ALIGNMENTS

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RESULT
AAV31987
ps-CAM; hown syndrome cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental relardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; mouse; ds; ss.
                                                                                                                                                                                                                Mouse bown syndrome-cell adhesion molecule DS-CAM 3' cDNA.
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                                                                                                                                                                                   aaacacacggacttcagatac 501
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Pred. No. 5.1e-148;
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CC neural cell adhesion molecules. A modified direct cDNA selection collection collection molecules. A modified direct cDNA selection collection collection collection collection collection collection details. A unique cDNA fragment, designated E51 (see AAV1982), was cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serven a trisomy 21 human foetal brain (14 wk cobtained and used to serve as deduced from coverlapping clones. A splice variant cDNA (see AAV31985), encoding coverlapping clones 900-1200 kb of genomic DNA and maps at chromosome compares spans 900-1200 kb of genomic DNA and maps at chromosome compares (see AAV31985-87), expression vectors and host cells, correspond to animals, antisense oligonucleotides, and primers useful correspond to the second of DS-CAM polypeptides are compared to severe developmental and neurological processes. They can be used in developmental and neurological abnormalities such as therapy of developmental and neurological abnormalities such as the corpus callosum, or schizencephaly. Antisense oligonucleotides created for inhibiting translation of mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DS-CAM1; Down syndrome-cell adhesion molecule; neural cell; signal transduction; trisomy 21; mental retardation; holoprosencephaly; corpus callosum agenesis; schizencephaly; diagnosis; assay; human; ds; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA clone codes for hown syndrome cell adhesion molecule DS-CAM1 (see AAW42086), a cell surface glycoprotein belonging to novel subclass of the 1g superfamily with highest homology to neural cell adhesion molecules. A modified direct cDNA select
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   develop products for detection, diagnosis and therapy of developmental and neurological abnormalities
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                                                                                                                                                                                                                                                                                                           Human Down syndrome-cell adhesion molecule DS-CAM probe
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                                                                                        Korenberg JR.
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Best Local Similarity
Matches 350; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and MXI. E51 was used as a probe to screen the trisomy 21 foetal brain library. 62 Clones were isolated from the 2 million clones of the original library. overlapping clones were obtained that were used to deduce a full-length sequence (see AAV31981) coding for novel hown syndrome-cell adhesion molecule DS-CAM1 (see AAW42086). A splice variant, DS-CAM2 (see AAV31988), was also identified. DS-CAM polypoptides are associated with developmental and neurological processes. The polypoptides and nucleic acids are used to develop products for the detection, diagnosis and therapy of developmental and neurological abnormalities.
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                                                                                       signal transduction; trisomy 21; me holoprosencephaly; corpus callosum schizencephaly; diagnosis; assay; l
                                                                                                                                                                                                         AAV31988;
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                                                                                                                             Down syndrome-cell adhesion molecule; neural cell;
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Best 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and is deleted for the entire transmembrane domain. The DS-CAM gene spans 900-1200 kb of genomic DNA and maps at chromosome 121q22.2-22.3. The invention also provides murine DS-CAM partial 21q22.2-22.3. The invention also provides murine DS-CAM partial sequences (see AAV31985-87), expression vectors and host cells, transgenic animals, antisense oligonucleotides, and primers useful for amplification of DS-CAM nucleic acid. DS-CAM polypeptides are associated with developmental and neurological processes. They can be used in e.g. neural prosthetic devices used in entubulation methods of repairing (regenerating) damaged or severed peripheral nerves. The products can also be used in detection, diagnosis and theraps of developmental and neurological abnormalities such as the products are also be used in detection, diagnosis and theraps of developmental and neurological abnormalities such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural cell adh-sion molecules. A modified direct cDMA selection technique was applied to bacterial and Plantificial chromosomes between ETS2 and MX1 by using cDNA from trisomy 21 human foetal brain. A unique cDNA fragment, designated E51 (see AAV31982), was obtained and used to screen a trisomy 21 human foetal brain (14-wk gestation) cDNA library. Further clones were obtained by exon trapping, and the complete DS-CAM2 cDNA sequence was identified trapping is a splice variant of membrane-bound DS-CAM1 (see AAW42086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Down's Syndrome-cell adhesion molecule develop products for detection, diagnosis and therapy developmental and neurological abnormalities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA clone codes for Down syndrome-cell adhesion morecure DS-CAM2 (see AAW42087), an extracellular, soluble protein belonging DS-CAM2 (see AAW42087), an extracellular, soluble highest homology to a novel subclass of the 1g superfamily with highest homology to neural cell adh-sion molecules. A modified direct CDNA selection neural cell adh-sion molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corpus callosum, or schizencephaly. Ant used for inhibiting translation of \mathfrak{mkNA}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA clone codes for Down syndrome-cell adhesion molecule
                                                                                                                                                                                                                                                     cggctgtccaatcacctcattcactcttgaatacayaccctttgggaccacggtctggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    syndrome, mental retardation, holoprosencephaly, agenesis of
                                 acttegecacqetgaaetaeqatggcagtacaateeete 279
                                                                                                                                                                                                                                   cggctgccccatcacctccttcacactagagtacaggccctttgggaccacagtttggac
                                                                                                                                                                                                                                                                                                               gctglttgccaycatcaacaccacacgcgtgaggclgaacctcattggctggaatgatgg
                                                                                                                                                                           cacagetcageggaectecetttecaagtectaacattetgtatgaectgeaagaageea
aagayyetgevadatgeaaagagtttagetgaaatuete 5175
                                                                          cctggtatgauntgcagatgcgggtgtgcaacagtgcgugctgngcggaqaagnagynta
                                                                                              cytuntatqaactqcagatgagagtgtgcaacaucyccugctgtucuqataagcaaucca
                                                                                                                                                        cacagetcagaggacetetetetecaagteet-acateetgtatgacetgcacgaageca
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Pred. No. 4e-46;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6413;
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RESULT
AAI 58196
21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; SHy-Drayer Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                          Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ 1D NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI58196 standard; cDNA;
                                                                                                  The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM4021-AAM42213) with nortropic, immunosuppressant and cytostatic activity. The polymiclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzeiner's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WU-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic;
                                                Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 399: 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; ss.
                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ
                          specification.
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QA,
                                                                                                                                                                                                                                                                                                                                  2001-442253/47.
                                     disorders.
The sequence data
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2000US-0598042
2000US-052931
2000US-0653450
2000US-0653191
2000US-0643036
2000US-0727344
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Wehrman T,
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                                      for this patent did
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Xu C, Xue AJ,
Drmanac RT;
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Yang Y,
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Query Match
Best Local Similarity
Matches 301; Conserv

Conservative

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Mismalches

Indels Length 5824;

27;

Gaps

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28.1%;

Score 140.8; DB 2 Pred. No. 4.4e-34;

22;

Sequence

5824

вр; 1298 А; 1942 С;

1580

G; 1004 T;

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other

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RESULT 6
AAC47995/c
ID AAC47995;
XX AAC47995;
AC AAC47995;
XX Hybridisa
Protein i
Protein i
KW metabolic
XX EP1033405
XX 106-SEP-20
XX 25-FEB-19
PR 05-MAR-19
PR 05-MAR-19
PR 05-MAR-19
PR 29-MAR-19
PR 29-MAR-19
PR 106-APR-19
PR 16-APR-19
PR 16-APR-19
PR 16-APR-19
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PR 11-APR-19
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05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

21-APR-1999

21-APR-1999
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 99US-0121825
99US-0123180
99US-0123548
99US-0125788
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99US-0126785
99US-0127462
99US-01287462
99US-0128714
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99US-013077
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       23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
11-MAY-1999;
11-MAY-1999;
11-MAY-1999;
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11-MAY-1999;
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5-JUL-1999;
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      990S-0130891
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990S-0134256
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990S-013427
990S-0135629
990S-0135629
990S-0135629
990S-0136782
990S-013463
990S-013463
990S-013463
990S-014683
990S-0146280
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990S-0146280
990S-0144333
990S-0144333
990S-0144333
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RESULT 7
AAC41871:
XX AAC41871:
XX AAC41871:
XX AC41871:
XX AAC41871:
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16-APR-1999

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99US-0161405
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9918-012548
9908-0125788
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9918-0126264
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14-OCT-1995; 14-OCT-1999;	13-OCT-1999; 13-OCT-1999;	13-0CT-1999;	08-OCT-1999;	07-0CT-1999;	05-OCT-1999;	04-OCT-1999;	28-SEP-1999;	24-SEP-1999;	22-SEP-1999;	20-SEP-1999;	15-SEP-1999;	13-SEP-1999;	07-SEP-1999;	01-SEP-1999;	30-AUG-1999; 31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	26-AUG-1999;	23-AUG-1999; 25-AUG-1999;	23-AUG-1999;	20-AUG-1999;	18-AUG-1999; 20-AUG-1999;	15-AUG-1999; 17-AUG-1999;	13-AUG-1999;	12-AUG-1999;	10-AUG-1999; 11-AUG-1999;	09-AUG-1999;	06-AUG-1999;	05-AUG-1999; 06-AUG-1999;	05-AUG-1999;	04-AUG-1999;	02-AUC-1999;	02-AUG-1999; 02-AUG-1999;	28-JUL-1999;	27-JUL-1999;	26-JUL-1999; 27-JUL-1999;	23-JUL-1999;	23-JUL-1999; 23-JUL-1999;	22-JUL-1799;	22-JUL-1999; 22-JUL-1999;	22-JUL-1999;	21-JUL-1999; 21-JUL-1999;	21-JUL-1999;
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              Ellis SB, Harpold MM,
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99US-0161404.
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99US-0161993.
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s-0160981.
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52.78;
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Pred. No. 0.41;
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                Campbell Kir:
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Best Local Similarity
Matches 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbit skeletal muscle calcium channel gamma-subunit-encoding cDNA - useful for identification of agonists-antagonists, design of therapeutic agents and diagnostic assays for e.g.
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25-FEB-1999
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01-APR-1999
01-APR-1999
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21-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAC53185 standard;
                                                                                                                                                                                                                                                                                                               Hybridisation assay: denetic mapping; gene expression control: protein identification; signal transduction pathway:
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                                                                                                                                                                                                                                                                                                     metabolic pathway: promoter:
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99US-0123180

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99US-0132407
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RESULT 11
AAV194
XX AAV194
AC AAV194
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XX Human
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XX Hepat
XX Amine
PT Humar
XX Amine
XX Clain
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The present sequence encodes a
                        Claim 3; Fig
                                             Amino acid sequence for liver/kidney microsome (LKM) l antibody human auto-immuno-hepatitis (AIH) type II and hepatitis C
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                                                                                                                                                                                                                                                                                                                                              cytochrome P450IId6; liver/kidney microsome; LKM-1; antibody; munohepatitis type II; AIH type II; hepatitis C virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; 585
                                                                                                                                                                                                                                                                                                                                                                                 P450IId6 encoding DNA 847-1431.
                                                                                                                                                                                                                                                                                                                           virus
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990S-0161405
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99US-0160989.
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1..585
/*tag: a
                        9pp;
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/transl_except= (pos:#16..318,aa:Xaa)
/note= "Xaa is unspecified"
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                          Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.8; DE pred. No. 1.9; O; Mismatches
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                                                                                                                       KK.
  protein fragment of cytochrome P450IId6
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which is recognised by AIH Type IIa/IIb LKM1 antibody. The antigens and their complementing antibodies are used in the detection of auto-immuno-hepatitis type II and hepatitis \mathbb C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human auxillary cytochrome
The nucleotide sequence of the cDNA coding region for the human auxillary cytochrome P450 species 2C6. The 96 to encodes a protein of 497 auxillary cytochrome P450 species 2C6. The 96 to encodes a protein of 497 amino acids. The cDNA was amplified by PCR uising the primers AQ87/63-6. The product was cloned into the yeast expression of the cytochrome P450 to produce the vectors P2D6 for the expression of the cytochrome P450 alone or p2D6R for co-expression with the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with recombinantly produced compound by reacting the chemical compound with resombinantly produced variants (AAQ87715), or 3A4 (AAQ87717) or their auxillary species and variants (AAQ87718), and yeast NADPH-P450 reductase, either as a fused variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused variants (AAQ8718-32), and yeast NADPH-P450 reductase, either as a fused variants (AAQ8718-32), and yeast NADPH-P450 reductase.
                                                                                                                                                                                                                                                       Evaluation expressing
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Yabusaki Y;
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20-JUL-1993;
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                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                         safety of a chemical cpd. - using recombinant yeast
man cytochrome p450 and a yeast NADPH-P450 reductase
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93JP-0201120.
93JP-0208279.
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Pred. No. 1.9;
0; Mismatches
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Best Local S
Matches 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1494
                                                                                                                                          Hayashi K,
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                                                                                                                                                                                                                                                                                                                                                       Human cytochrome P450; amplification; PCK; yeast NADPH-P450 reductase; safety; fusior carcinogen; mutagen; liver metabolism; ds.
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                                                                                                                                                                                                                                                                                                                                                                                         Human auxillary cytochrome
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                                                                                                                                                                                                                                                                                                             variation
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                                                                                                                                                                                                              21-JUL-1993;
                                                                                                                                                                                                                               20-.101.-1994;
                                                                                                                                                                                              30-JUL-1993;
                                                                                                                                                                                                       20-JUL-1943;
                                                                     Examples; Page 87-89; 124pp; English.
                                                                                     expressing
                                                                                                Evaluation
                                                                                                                 P-PSDB;
                                                                                                                         WPI; 1995-116991/16
                                                                                                                                                                    (HAYA/) HAYASHI K.
(SUMO ) SUMITOMO CHEM CO LTD.
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                                                                                    of satety of a chemical cpd.
human cytochrome p450 and a
                                                                                                                                                   Kaneko H,
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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886
                                                                                                                                                                                                                                                                                                                                                                p450; amplification; PCR; primer; expression vector; reductase; safety; fusion protein; metabolite;
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61.9%;
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                                                                                         yeast NADPH-P450 reductase
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The nucleotide sequence of the CDNA coding region for the human auxillary cytochrome P450 species 2D6 variant 1. The gene contains a change at base 886 from T to C as compared to the wild type sequence (AAQ87729). This changes the amino acid residue 296 from Cys to Arg. The CDNA was amplified by PCR using the primers AAQ87763-6. The product was cloned into the yeast expression vectors pAAH5N or pAHRR to produce the vectors p2D6 variant 1 for the expression of the cytochrome P450 alone

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RESULT 14
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11D AAQ877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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hes 52; Conserv
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20-JUL-1993;
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Yabusaki Y;
                           P-PSDB; AAR72377
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                                                                                                                                                                                                           HAYASHI K.
                                                                                                                                                                                     SUMITOMO CHEM
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                                                                                                                                    Kaneko H,
                                                                                                                                                                                                                                                             93JP-0180246.
93JP-0201120.
93JP-0208279.
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886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             b
"C to G change
acid from Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "T to C change in variant acid from Cys to Arg"
                                                                                                                                         Komai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
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sm; ds.
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Ser"
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protein; metabolite;
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CC converted into a carcinogenic or mutagenic form the human converted into a carcinogen passes the safety of the chemical compound. The method is useful for cases the safety of the chemical compound, or in cell extracts, and years the resulting method into a carcinogene protein or in cell extracts, and years the compound. The method is useful for cases the safety of a chemical compound, or in cell extracts, and years the protein or their awaillars for the cases the safety of a chemical compound. The method to reductase.
                                                                                                                                                                                                                                                                                                                                Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
                                                                                                                                                                                                                                                                                                           124pp; English.
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Sequence

1494

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248

A: 508 C;

447

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291 T; 0 other;

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AAQ87732
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Best Local
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         21-JUL-1993;
20-JUL-1993;
30-JUL-1993;
                                                                                                                                                                                                                                                                ANQ87732 standard; cDNA; 1494 BP
                                                                                                                                                                                                         Human auxillary cytochrome P450 species 2D6 variant 3 coding region.
                                                                                                                                    Key
                                                                                                                                                      Homo
                                                                                                                                                                        carcinogen;
                                                                                                                                                                                 Human cytochrome P450; amplificatio
yeast NADPH-P450 reductase; safety;
                                                                                                                                                                                                                             15-NOV-1995
                                                                                                                                                                                                                                                                                                                                405
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                                                                                                                           variation
                                            20-JUL-1994;
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mes 52; Conserv
                                                                                                                                                                                                                                                                                                                      tgcggangagacggcgagancaga 428
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milarity 61.9%;
Conservative
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                                                                                                                                                                         mutagen;
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          93JP-0180246.
93JP-0201120.
93JP-0208279.
                                             94EP-0111298
                                                                                                                            Location/qualifiers
1457
                                                                                                          /note-
                                                                                                                                                                          liver metabolism;
                                                                                                                                                                                            amplification; PCR;
                                                                                                   a
"C to G change in variant 1 changes amino
acid from Thr to Ser"
                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred.
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                                                                                                                                                                                     tusion
                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                    primer; expression vector;
protein; metabolite;
                                                                                                                                                                                                                                                                                                                                                                                        32;
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CC change at base 1457 from C to G as compared to the wild type sequence of the CDNA coding region for the human CC change at base 1457 from C to G as compared to the wild type sequence CC change at base 1457 from C to G as compared to the wild type sequence CC change at base 1457 from C to G as compared to the wild type sequence CC cDNA was amplified by PCR using the primers AAO87763-6. The product was CC cDNA was amplified by PCR using the primers AAO87763-6. The product was compared into the yeast expression vectors AAO87763-6. The produce the vectors p2D6 v.riant 3 for the expression of the cyto-hrome P450 alone or p2D6R variant 3 for co-expression with the yeast NADPH-P450 cor pedBR variant 3 for co-expression with the yeast NADPH-P450 of reductase. The vectors are used in a method for evaluating the safety of CC produced human cytochrome P450 molecular species 1A2 (AAO87714), 2C9 cc produced human cytochrome P450 molecular species 1A2 (AAO87714), 2C9 cc (AAO87715), 2E1 (AAO87715), or 3A4 (AAO87717) or their auxillary species CC (AAO87715), 2E1 (AAO87718-32), and yeast NADPH-P450 reductase, either as a cc and variants (AAO87718-32), and yeast NADPH-P450 reductase, either as a cc fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabol will be converted into a carcinogenic or mutagenic form through metabolism in the
                                                                                                                                                         Qγ
                                                                                                                                                                                                          Dβ
                                                                                                                                                                                                                                                 Ş
                                                                                                                Db
Search completed: March 4, 2002, 05:24:09 Job time: 17678 sec
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluation of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase
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P-PSDB; AAR72378.
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Yabusaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; Page 95-97; 124pp; English.
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(SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1494 BP; 248 A; 507 C; 447 G; 292 T; 0 other;
                                                                                                                                        405 tgcggaggagacggcgagagcaga 428
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                                                                                                             tgcagegecytyleeaacaggaga 1003
                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                      ; Score 32.8; D; pred. No. 3; 0; Mismatches
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Maximum DB
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nucleic search, using sw model
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/5B_CUMH.seq:*
/cgn2_6/ptodata/2/ina/66_CUMH.seq:*
/cgn2_6/ptodata/2/ina/66_CUMH.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_CUMH.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_CUMH.seq:*
                  Gapext 1.0
US-08-123-161A-11
US-08-48+-278-11
US-08-910-864-11
5482709-5
5273901-6
5273901-6
145-658D-25
US-08-36-074-54
PCT-US96-06352-81
US-08-145-658D-24
US-08-145-658D-24
US-08-145-658D-24
US-08-145-658D-22
US-08-145-658D-22
US-08-145-658D-22
US-08-145-658D-20
US-08-267-803B-1
US-08-267-803B-1
US-08-267-803B-1
US-08-267-803B-1
US-08-267-803B-1
US-08-728-323A-1
US-08-728-323A-1
US-08-728-323A-1
US-08-728-323A-1
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5386025-1
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499.870 Million cell updates/sec
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                                                                                                                                                                              Patent No. 5386025
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
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Patent No. 5273901
                    Sequence 2, Appli
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US-08-336-257A-1
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229
310
310
313
323
333
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340
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jay, Scott D
APPLICANT: Ellis, Steven B.
APPLICANT: Halpold, Michael M.
APPLICANT: Camphell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES:
B CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Mailin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IHM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                 FEATURE:
                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                  NAME: Soldman, Stephante L. REGISTRATION NUMBER: 53,779
REFERENCE/LOCKET NUMBER: 54898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: USA
ZIP: 92101-2926
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 07-NOV-1994
CLASSIFICATION: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1660 Un
CITY: San Diego
              LOCATION: 49..717
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                         TOPOLOGY:
                                                      NAME/KEY: CDS
LOCATION: 49.
                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                LENGTH:
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calcium channel"
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US-08-145-658D-21
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US-09-115-446-1
US-09-115-446-5
US-09-115-446-5
US-08-899-595-4
US-08-899-595-9
US-08-301-162-9
US-08-424-268-7
US-08-424-268-7
US-08-424-268-7
US-07-863-169A-6
US-08-429-964-6
US-08-428-7
US-07-935-087-6
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US-08-188-277B-6
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Query Match

6.78;

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Length 1171;

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5386025-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Patent No. 5386025; APPLICANT: JAY, STOTT D.;ELLIS, STEVEN B.;HARPOLD, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/08123161A ; Patent No. 5449616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-123-161A-11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: HIM PC compatible
OPERATING SYSTEM: PC-POS/MS-TOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, Richard D. APPLICANT: Ibrashimov, Oxana B.
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ibradhimov
APPLICANT: Yand, Bin
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                                              PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                 STREET: P.O. Box
CITY: York Harbor
STATE: ME
                                                           FILING DATE: 16-SEP
CLASSIFICATION: 435
                                                                                                                                                                                                                ZIP: 03911
                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                 ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Rox 999
            APPLICATION NUMBER: 07/946,234 FILING DATE: 14-SEP-92
                                                                                             APPLICATION NUMBER: US/08/123, 161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                    NSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campbell,
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                                                                           16-SEP-93
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60.2%;
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US-08-483-278-11
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REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIRF
TELECOMMUNICATION INFORMATION:
TELEPIONE: (207) 363-0528
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 11:
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Best Local Similarity 58.9%;
Matches 56; Conservative
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Patent No. !
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                TELEFAX: (207) 363-0528 INFORMATION FOR SEQ ID NO: 11:
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LENGTH: 1396 base pairs
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                                                            FILING DATE: 16-SEP-93
AUTORNEY/AGENT INFORMATION:
NAME: FEITE-IL KEVIN M.
REGISTRATION UNMBER: 45,505
REFERENCE/DOCKET NUMBER: UIKE89-11A5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                          COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC 1005/MS 1005
SOFTWARE: Patenth: Release #1.0, Version #1.25
                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
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                                                                                                                                                                                                        CLASSIFICATION: 435
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                                                                                                                                                                     APPLICATION NUMBER: 08/123, 161
                                                 TELEPHONE:
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WENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
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                                                    (207) 363-0558
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Pred. No. 0.61;
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US-08-483-278-11
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Dest Local Similarity 58.9
Matches 56; Conservative
                                  US-08-910-864-11
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ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A CDNA OF AN EXTREMELY TITLE OF INVENTION: SMALL QUANTITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin kel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: 619-678-5070
                                                                                                                                                                                                                                                                                       FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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LENGTH: 14% base pair
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                FEATURE:
                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DUS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                           NAME: HATLE, LISA A. REGISTRATION NUMBER: 38,347
                                                                                                                                           : SdAd
                                                               NAME/KEY:
                                                                                                           : YOUTOGY:
                                                                                                                         STRANDEDNESS: double
                                                    LOCATION:
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                                                                                                                                    nucleic acid
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                                                                                                                                                         143 base pairs
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                                                                                                              linear
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16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                           OMBER: US/08/910,864
13-AUG-1997
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58.9%;
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DB 4:
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 Length 1446;
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Query Match

6.5%; Score 12.6;

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5482709-5/c
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; TITLE OF INVENTION: EINERIA ANTIGENIC COMPOSITION WHICH
;ELICITS ANTIHODIES AGAINST AVIAN COCCIDIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JACOBSON, JAMES W.: STRAUSBERG, ROBERT L.: WILSON, ;SUSAN D.: POPE, SHARON H.: STRAUSBERG, SUSAN L.: RUFF, MICHAEL D.:
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                                                                                                                                                                                                                                                                                                                                  RESULT 7
5273901-6/c
; Patent No. 5273901
                                                                                                                                                                                                                                                                             APPLICANT: JACONSON, JAMES W.:SIKAUSHERG, KOBERT L.:WILSON, ;SUSAN D.:POPE, SHAKON H.:STKAUSHERG, SUSAN L.:KUFF,MICHAEL D.:;AUGUSTINE, PATKICIA C.:HANFORTH, HARRY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:5:
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5273901-6
                                                                                                                                                                                                                              SPOROZOITE 21.5 KB ANTIGEN, AC-6B
NUMBER OF SEQUENCES: 11
                                SEQ ID NO:6:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215, 162
FILING DATE: 05-JHL-1988
                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               974 GPCATGPGCCGGCGGGGGGGAGAAGGCTGAAGAG 1008
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FILING DATE: 05-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-SEP-1990
                                                                                                                                                                        APPLICATION NUMBER: US/01/581,693
FILING DATE: 12-SEP-1990
                                               FILING DATE: 05-JUL-1984
                                                                  FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
                                                                                                    APPLICATION NUMBER: 746,520
             LENGTH: 54 3
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19-JUN-1985
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Pred. No. 0.65;
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Best Local Similarity
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Best Local Similarity 60.3
K. tches 51: Conservative
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                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 23:
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APPLICATION NUMBER: US/08/145,658D
FILING DATE: 04-NOV-1993
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                                                                                                                                                                                                                                                           NAME: Brudy, Jr., James W.
REGISTRATION NUMBER: 32.115
REFERENCE/DOCKET NUMBER: E8280.017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
TELEPAX: 202-887-0689
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: GB 9001181.8
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OPERATING SYSTEM: PC-108/MS-108
SOFTWARE: Patentin Release #1.0, Version #1.40
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STATE: DC
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STRANDEDNESS: single
                                                                                         ORGANISM:
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                 6.2%;
Similarity 60.7%;
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      Score 31.2; bi
Pred. No. 1.9;
O; Mismatches
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: Patent No. 5705443
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Best Local Similarity 53.3%;
Matches 65; Conservative
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APPLICANT: FEDEK, JOHN N.
APPLICANT: GNIKKE, ANDREAS
APPLICANT: THOMAS, MINSTON J.
APPLICANT: WHIFF, ROCER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                               454 qa 455
                                                                                                                                                                                  394 Tetaertaattataenaanhaaaacayenadagecaaayaggetyagayatgeaaa 453
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REFERENCE/DOCKET NUMBER: 9053 0001.21
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421 GA 422
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TELEFAX: (202) 887-0763
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STRANDEDNISS: sincic
TOPOLOGY: linear
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N: 435
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US-08-436-074-54
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                                                                        RESULT 11
PCT-US96-06352-81
Sequence 81, Application PC/FUS9606352
GENERAL INFORMATION:
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TITLE OF INVENTION: HEMOCHROMATUSIS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       st Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KIMMET, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 90 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                          APPLICANT:
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TELEFAX: 90-4030
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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5753438
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                          DRAYNA, DENNIS T. FEDER, JOHN N. GNIKKE, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (202) 887-1500
(202) 887-0763
             KIMMEL,
                                                                                                                                                                                                                                                                                                                                           Conservative
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53.3%;
                 BRUCE E
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pred. No. 2;
0; Mismatches 57;
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PCT-US96-06583-81
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INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
EILING DATE: 09-FEB-1996
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OPERATING SYSTEM: PRIDES/MS-DAS
SOFTWARE: Patentin Recease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: MORRISON & FOERSTER
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TITLE OF INVENTION: METHOD TO DIAGNOTITLE OF INVENTION: HEMOCHROMATOSIS
                                                                 APPLICAVE: DRAYNA, DENNIS F.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIRKE, ANDEAS
APPLICANT: KIMMEL, BRUCE F.
APPLICANT: THOMAS, MINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
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                                CORRESPONDENCE ADDRESS
                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GCCCAAGGTATTGGTGAGGTTGGCAGTGTGGCTGCTGGTGGGGGCTGTGGCCCTCTCTGCT 360
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    361 TETETIGGGCTETIGEAGGTECTIGCTIGCTIGGT FCT ACCCCTGCTGCAGAAGAAAGATGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                   ADDRESSEE:
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2000 Pennsylvania Ave. N.W., Suite
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                   MORRISON & FOEKSTER
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Fred. No. 2;
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20006-1888

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Best Local Similarity 53.3%;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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FILING DATE: 09-FEB-1996
ANTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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421 GA 422
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TELEFAX: 90-4030
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COMPUTEK: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-INOS
COMPUTER DISCONSIDERATIONS
COMPUTER DISCONSIDERATIONS
CONTRACTOR OF THE PC-DOS/MS-INOS
CONTRACTOR OF THE PC-DOS/
                   OPERATING SYSTEM: LOS
SOETWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29,959
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                                                                                                                                                               IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30.8; DB 5; Length 1050; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
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Best Local Similarity 56.4%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08145658D Patent No. 5981174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                              МЕННИМ ТУРЕ: Floppy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2138 GAACCCEATGCTTTCGTTGTLGCTCCCCTTGCTGGTGGTGGAGGAAAGAAGAACGA 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wolf, Charles R. APPLICANT: Miles, John S. APPLICANT: Sput, Nigel K. APPLICANT: Gough, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
                                                                                                        FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/732,223
                                                                                                                                                                                                       APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GEN FIG ASSAY NUMBER OF SEQUENCES: 2'
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                                                  NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 42,115
REFERENCE/DOCKET NUMBER: E8280.017
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Washington
STATE: DC
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REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 46
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                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 FILING DATE: 04-NOV 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
              TELEPHONE:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08145658D Patent No. 5981174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDN HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wolf, Charles R.
APPLICANT: Spurr, Nigel K.
APPLICANT: Spurr, Nigel K.
APPLICANT: Gough, Alan C.
APPLICANT: Gough, Alan C.
TITLE OF INVENTION: GENETIC ASSAY
NUMBER OF SEQUENCES: 25
COKRESPONDENCE ADDRESS:
                                                                                                                            TELEFAX: 202-887-0689
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CITY: Washington
CITY: DC
CTATE: DC
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TYPE: n
TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                         NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32.115
REFERENCE/DOCKET NUMBER: E8280.017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-785-9700
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: GB 9001181.8
APPLICATION NUMBER: GB 9001181.8
FILING DATE: 18-JAN-1990
PRIOR APPLICATION NUMBER: US 07/732,224
APPLICATION NUMBER: US 07/732,224
FILING DATE: 18-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       979 TGCAGCGCCGTGTCCAACAG 998
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1566 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 04-NO
CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP
2101 L Street N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wolf, Charles R.
                                                                                                                                           202-887-0689
                                    Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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                     CDNA to mRNA
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US-08-145-658D-13
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Search completed: March 4, 2002, 05:13:00 Job time: 17034~{\rm sec}
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Best Local Similarity 63.9%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 Legigarealereetgealeriggieggggtletaetgelotilgigettetgelgglig 404
| Hilli III | Hill | Hil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          980 TIGCAGCCGTIGTC 991
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